3564, Ap 461, Ap 461, Ap 1267, Ap 1267, Ap 1583, Ap 137, App 137, App 16, App 1250, Ap 166, Ap 166, Ap 166, Ap 166, Ap

Sequence 3 Sequence 5 Sequence 2

Sequence 1 Sequence 1 Sequence 1 Sequence 3

Sequence 2 Sequence 5 Sequence 3

Sequence 3 Sequence 3 Sequence 5 Sequence 1

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Sequence 355, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
GIL H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER HP Vectra 486/33 OPENATES: BY Vectra 486/33 OPENATES: ASCII Text SOFTWARE: ASCII Text CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E FILING DATE: 20-Oct-1997 CLASSIFICATION OFFER: 60/009,861 FILING DATE: January 5, 1996 APPLICATION NUMBER: 60/009,861 FILING DATE: January 5, 1996 APPLICATION NUMBER: 60/009,861 FILING DATE: January 5, 1996 APPLICATION NUMBER: 08/781,986 FILING DATE: January 3, 1997 ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
US-09-710-279-3348

US-09-710-279-4042

US-09-543-681A-2690

US-09-543-681A-2690

US-09-902-540-2208

US-09-902-540-2208

US-09-902-540-1583

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US-09-134-000C-937

US-09-134-000C-937

US-09-134-0012-2023

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US-09-107-433-2206

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Sequence 15, Appl
Sequence 15, Appl
Sequence 238, Appl
Sequence 238, Appl
Sequence 604, Appl
Sequence 604, Appl
Sequence 2556, Apl
Sequence 2556, Apl
Sequence 862, Apl
Sequence 862, Apl
Sequence 862, Apl
                                                                               November 9, 2005, 12:50:22 ; Search time 214 Seconds (without alignments) 2561.461 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-781-986A-355
US-09-830-217-15
US-10-278-946-15
US-08-956-171E-238
US-08-781-986A-238
US-08-956-171E-604
US-08-956-171E-2556
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US-09-134-001C-2655
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Listing first 45 summaries
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9 Sequence 355, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICATY: Charles Kunach

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCES: 5255

CORRESPONDENCES: 5255

CORRESPONDENCES: 5255

CORPESSEE: Human Genome Sciences, Inc.

STREET: 9410 key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER: HP Vectra 486/33

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 355:
                                                                                                         LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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475.00
86.89$
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Best Local Similarity:
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182 CATGCTAAAAAGATTCTGCTGAATTCAAGAAGTTACAAGAAGATGCAACATGGAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: PR461PCT
CURRENT APPLICATION NUMBER: US/09/830,217
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: PCT/US99/06199
PRIOR APPLICATION NUMBER: 60/080,296
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-04-01
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Matches:
Conservative:
Mismatches:
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US/08/781,986A
    APPLICATION DATE:
FILING DATE:
CLASSIETCATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
STRANDEDNESS: double
STRANDEDNESS: double
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86.89%
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APPLICATION NUMBER:
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 ---TCTACTGATACAGTTTTCAAATTCAAA---GATACAACTAAGTTAATGGGGAAAGCT 480
                                                                                                                                                                                                            19 ATTAAAATGCTT---GTTGTTACGCTTGCTTTCCTACTTGTT---TTAGCAGATGTAGT 72
                                                                                                                                                                                                                                       28 AsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis 47
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541 TTCCAAAAA-----GATGCAAAGCAAAGTATAAAGATGCCATTGAAA 588
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                                                                                                                                                                                                8 Leulys11eleuServal11eGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGly
                                                                                                                                                                                                                                                                             48 GluGluGlyThrThrLysValProLysHisProLysArgValValLeuGluTyrSer
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 60/084,674
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 999
                                                           ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-830-217-15
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51.74%
32.85%
23.96%
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Best Local Similarity:
Query Match:
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Leu------LysGluLeuGluLysAspProValTrpLysLysLeuAsnAla 292
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811 TTAGTTAAAAAGACTGAAAGCGAATGACTTCAAGTAAAGAGTGGAAAAATTTAGACGGA 870
                                                                                                                                         293 ValLysAsnGlnArgVal----AspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
                                                                                                                                                                 312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys 331
                                                                                                                                                                                                                                                     931 TATAAATCTTCATTAAAACTTATTGACGATTTATATGAA------AAGTTAAATGAA 984
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73 GGGAATTCAAATAAACAATCATCATAACAAAGATAAGGAAACAACTTCAATTAAACAT 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Simpson et al.

TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: P846,1USD1
CURRENT APPLICATION NUMBER: US/10/278,946
CURRENT APPLICATION NUMBER: US/10/278,946
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: PCT/US99/06199
PRIOR PILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: US 60/078,682
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
CONTWARE: Patentin Version 3.1
SEQ ID NO 15
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                            US-10-278-946-15; Sequence 15, Application US/10278946; Patent No. 6821754; GENERAL INFORMATION:
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405.00
51.74%
32.85%
23.96%
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985 AAACAATCAAAA 996
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Best Local Similarity:
Query Match:
DB:
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Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VallyeAenGlnArgVal -- - AspileLeuAspArgAspLeuTrpAlaArgSerArgGly 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691 CAAAAACAAGTIGATAATGGTAAAGATATTATCCAACTTACATCTAAAAGAAGCATTCCA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 GlnValAsnProGluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSer 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::||| ::: | ::: | :::||||::::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::
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LysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSerValGlyThr 107
                                                                                                            108 ArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAsp 127
                                                                                                                                                               GAACCTGCACCTAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCA 372
                                                                                                                                                                                                                    128 AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysileAlaProThrIleGluLeu 147
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                                                       253 CAAAAACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
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US-08-956-171E-238
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CITY: Rockville

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148 LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla 167
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                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3775
113
65
132
34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
                                                                                                                                                                                    FILING DATE: 20-Oct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      NAME: Mark J. Hyman
REGISTRATION WNDER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO: 238
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO. 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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405.00
51.74%
32.85%
23.96%
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Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-956-171E-238
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TELEPHONE: (301) 309-8504
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
         TELECOMMUNICATION INFORMATION
                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                               US-08-781-986A-238
                                                                                                                                        Alignment Scores:
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---TCTACTGATACAGTTTTCAAATTCAAA---GATACAACTAAGTTAATGGGGAAAGCT 522
                       LeuGlylysysiysiugluglyLysLysArgLeuGluGluHisAspLysLysIleGluGlu 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 238, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                       TyrLysLysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                      :::::|||
583 TTCCAAAAA--------GATGCAAAAGCAAAGTATAAAGATGCCATTGAAA
                                                                                                                                    221 GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu
                                                                                                                                                                                             -----AATAAGACTTA
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                                                                                                                                                                                                                                                                                                            Leu-------LysGluLeuGluLysAspProValTrpLysLysLeuAsnAla
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691 GAAATCTTAAATGATTTAGGATTCAAACGT------
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                     208 SerGlyLeuLeuAlaHisProSerAsn-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
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|1027 AAACAATCAAAA 1038
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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61 ATTAAAATGCTT---GTTGTTACGCTTGCTTTCCTACTTGTT---TTAGCAGGATGTAGT 114
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                                                                                                                                                                                                                                                          28 AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis
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      3775
113
65
132
34
                                                                                                                                     US-10-724-972A-6352 (1-335) x US-08-781-986A-238 (1-3775)
                        Matches:
Conservative:
Mismatches:
Indels:
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        Length:
5.58e-36
405.00
51.74%
32.85%
23.96%
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------ATTGATCCTGCAGTTTGGAAATCATTAAAA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 SerAsnGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLysLeuAsn 291
                                                                                                                                                                                                                                                                                                             123 CAGAGTACGTTAAAATCTGCATTTGCATTCGGTATCTCAAGAGCAGGTATGTTTATTAAT 182
                                                                                                                                                                                                                                                                                                                                                                          234 AspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 MetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHis 213
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TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                            154 TyrasnGluasnIleaspalapheLysThrIleSerLysalaLeuGlyLysGluGluGlu 173
                                                                                                                                                                                                     174 GlyLyslysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThr
                                                                                                                                                                                                                                                                                                                                                   214 ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSer
                                                                                                                                                 312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
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                                                                                          US-10-724-972A-6352 (1-335) x US-08-956-171E-604 (1-2115)
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Conservative:
Mismatches:
Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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US-08-781-986A-604
; Sequence 604, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
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ATTORNEY/AGBNT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
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     63.84%
37.85%
19.76%
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CURRENT APPLICATION DA
APPLICATION NUMBER:
       Percent Similarity:
Best Local Similarity:
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                                                                                                         293 yaliyaanginargyal---AsplieleuaspargaspleuTrpalaargserargGly 311
           GlnValAsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSer 277
                                                                                    ----LysGluLeuGluLysAspProValTrpLysLysLeuAsnAla 292
                                            793 TTAATGAACGCTGATCATATTTTTGTAGTAAAATCGAAATGCGAAAGATGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and NUMBER OF SEQUENCES: 5256
CORRESPONDENCE: 5256
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-00c-1997
CLASSIFICATION: UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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REGISTARION UNDBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-956-171E-604
Sequence 604, Application US/08956171E
Sequence 100. 6593114
GENERAL INFORMATION:
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HATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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Gil H. Choi
                                                                                                                                                                                                                                                                                                                                          1027 AAACAATCAAAA 1038
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Pred. No.:
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Alignment Scores:
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Patent No. 6593114
GENERAL INFORMATION:
GENERAL INFORMATION:
GIL H. Choi
GIL H. Choi
Crail A. Robern
Steven C. Barsh
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                        154 TyrkenGlukenilekepalaPheLyeThrIleSerLyeAlaLeuGlyLyeGluGluGlu 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 MetAsplysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHis 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 AATGAAGATACATTTAFGGGACAATTCTTAATTAAAATGGGTATTCAACCTGAAGTCANA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSer 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 GluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsn---LysAlaSer 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| |||::: :::||||||::: ||| 303 GAAGAACTTGCCAATGATTTTAGCCACTGACGGAAAACGGAC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470
                                                                                                                                                                                                                                                                                                                                                                                                             273 SerAsnGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLeuAsn 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 AAAAATAGAAGGAAATTC------ATTGATCCTGCAGTTTGGAAATCATTAAAA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 GlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||||:: :::||||
411 GCTGTGAAAGATAACAAAGTTTATGACGTTGACCGAAATAAGTGGTTGAAATCAAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AlavalLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeulleSerSerGluGluMetAlaLyBGluLeuValGluLeuSerLyBLyB
                                                                                                                                                                                                                                                                                                                                                   US-10-724-972A-6352 (1-335) x US-08-781-986A-604 (1-2115)
                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
          PB248PP
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                3.35e-28
334.00
63.84%
37.85%
                                                                                                                                                double
                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                         TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                  US-08-781-986A-604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-956-171E-2556
                                                                                                                                                                                                               Alignment Scores:
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DB:
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ArgIleIleLvsProLeuArgAspLysIleGlyLysTyrThrSerValGlyThrArgLys 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 ArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-701-966A-2556
Sequence 2556, Application US/08781986A
Sequence 2556, Application US/0878196A
Sequence 2556, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
APPLICATION NUMBER: 60/199,861
APPLICATION NUMBER: 08/781,986
APPLICATION THORMATION:
ATTORNEY AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SRQUENCE DESCRIPTION: SEQ ID NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.68e-29
333.00
90.00%
82.50%
19.70%
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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117 SerLysLeuLysProAspLeullelleAlaAspAsnAsnArgHisLysGlylleTyrLys 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 GAAACTACATTGACGATAAACAGATAGTAATGGAGACCAAATCGAGGTGCCAAATAATCCA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 AsplysileGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluile 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 ---LygProValGlylleAlaAspAsnLysLysAsnArglleIleLysProLeuArg 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 ValArgGlyLeuLysIleLeuSerVallleGlyLeuLeuPheValLeuIleAlaThrAla 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaCysGly-----AsnAsnSerSerSerAsnSerSerLysGluSerSer----- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysAspGlyValGluIleLysHisGluGluGly---ThrThrLysValProLysHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 LysArgvalvalvalLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-724-972A-6352 (1-335) x US-09-107-532A-862 (1-1059)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
                              CURKENI APLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/08151
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATINIBALIO, PARMELA DENEKE
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1059
SEQUENCE DESCRIPTION: SEQ ID NO: 862:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-507
TELEPAX: (781)893-827
INFORMATION FOR SEQ ID NO: 862:
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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307.50
50.29$
31.29$
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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Sequence 862, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 ArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 ArgileileiysProLeuArgAspLysileGlyLysTyrThrServalGlyThrArgLys 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 GlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 CGTATCATTAAACCAGTTAGAGAAAAATTGGGGATTATACTTCTGTAGGTACACGTAAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GATGCATTAGCAGCATTAGACGTTAAACCAGTTGGTATTGCTGATGATGGTAAAAAAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 AspalaleuvalalaleuaspvallysProvalGlyilealaaspaspasnLysLysAsn 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-724-972A-6352 (1-335) x US-08-781-986A-2556 (1-242)
                        MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/781,986A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Benean, BOD
REGISTRATION NUMBER: 30,446
REPERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPAN: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISCIS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.68e-29
333.00
90.00%
82.50%
19.70%
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-107-532A-862
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1059 107 65 123 173

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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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DB: 3 Gaps: 16 US-10-724-972A-6352 (1-335) x US-09-134-001C-2655 (1-1056) US-10-724-972A-6352 (1-335) x US-09-134-001C-2655 (1-1056) US-10-724-972A-6352 (1-335) x US-09-134-001C-2655 (1-1056) US-10-724-972A-631 US-09-134-001C-2655 (1-1056) US-10-724-972A-631 US-09-134-001C-2655 (1-1056) US-10-724-972A-631 US-09-134-001C-2655 (1-1056) US-08-10-10-10-10-10-10-10-10-10-10-10-10-10-	LeuGluTyrSerPheValAspalaLeuValAlaLeuAspValLysProValGlyIleAla ::: ::	Qy 116 IleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsnAsnAsnAsnAsnAsnAslyIle 134 Db 406 GTTGCATCAGCTAAACCAGATGTGATTTTTATTTCAGGAAGAACAGTAATCAGAAAAAT 465 Qy 135 TyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysSerPheAspGlyAspTyr 154 Db 466 TTAGATGAATTTAAAAAAGCTGCACCAAAAGCTAAAGTTGTATATGTAGGTACAAGT 522 Qy 155 AsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLeuGly 169 Db 523 GATGACAACTTAATTAAAAAAAAAAAAAAAAAAAAAATTAAGGGAAAAATTAAGGAAAAATTAAGGAAAAATTAAGGAAAAATTAAGGAAAAATTAAAGAAAAAA	170 LysGluGluGluGlyLysLysBleuGluGluHisAspLysLysIleGluGluTyrLys 189	Oy 249 LeuglnMethanThrGluThrLeuSerGlnValAsnPro
Qy 137 AspLeuAsnLysIleAlaProThrIleGluLeuLysSerPheAspGly	232 L 232 L 784 - 248 T 820 - 871 G		1C-2655 636, Applicate 6365, Applicate 6380300 FORWATION: IN LYAIN DOUCETINEWRITON: INVENTION: INVE	SEQ ID NO 2655 SEQ ID NOS: 5674

601

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RESULT 14
US-09-10-279-4042

is Sequence 4042, Application US/09710279
; Sequence 4042, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT; KIMBRILY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4042
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysGlualaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyr 248
                                                                                                                                                                                                                                                                                                                                           262 GluargMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu 281
                                                                                                                                                                                                                                                                                                                                                                                                           444 GATCGTGGTTCAGTTGTAAGGGAACAACAAAT--------CAAGTT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                        282 GlulysAspProvalTrplysLysLeuAsnAlavalLysAsnGlnArgValAspIleLeu 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGlu 321
                                                                                                                                                                                                                                                                                              ..... 261
TTAGATGAATTTAAAAAGCTGCACCAAAAGCTAAAGTT---GTATATGTAGGTACAAGT 778
                                                                                                                                                     LysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGly 209
                                                                                                                                                                        LeuLeuAlaHis---ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPhe
                                                                                                                                                                                                                                      CTATCAACGTITGGACCAAGAAGATTGGTGGTTTAGTGTTTTGATACATTAGGATTT
                                      AsnGluAsnIle-----AspAlaPheLys-----ThrIleSerLysAlaLeuGly
                                                                  GATGACAACTTAATTAAAGATATGAAAAATACAGAAAATTTAGGGAAAATCTACGAT
                                                                                               LysGiuGluGluGlyLysLysArgLeuGluGluHisAspLysLysLyslieGluGluTyrLys
                                                                                                                 Description of Artificial Sequence: synthetic nucleic acid sequence
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ORGANISM: Artificial Sequence
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| 1299 GGAGTTGCACATATGAAAAAAACAGTCTTATTTTTTATTGTTGTCTCTAGTTTTAGTTTTA 1240
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        ---TCTTCAACGACAACTATCAAACAA 1014
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                                                                                                                           Sequence 3.48. Application US/09710279
| Sequence 3.48. Application US/09710279
| Patent No. 6703492
| GENERAL INFORMATION:
| APPLICANT: KIMMERLY, WILLIAM JOHN
| TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
| TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
| CURRENT FILING DATE: P03480US
| CURRENT FILING DATE: 1999-11-09
| PRIOR PILING DATE: 1999-11-09
| NUMBER OF SEQ ID NOS: 4472
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 3348
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US-09-710-279-3348
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US-10-	US-10-724-972A-6352 (1-335) x US-09-710-279-4042 (1-3267)	Db 1649 GATCCAAAACTATGGTATTTCTCTTCAGGATCTTCAACGACAACTATCAAACAA 1702
ે. જે લે	1 GlyValGluSerValArgGlyLeuLygIleLeuSerValIleGlyLeuLeuPheValLeu 20	Qy 322 LeuValGluLeuSerLys 327 :::
රු සි	21 IlealaThralaalaCysGlyAsnAsnSerSerSerAsnSerSerLysGluSerSer 39	RESULT 15 US-09-710-279-3564 Sequence 3564, Application US/09710279
දු පු		GENERAL INFORMATION: APPLICANT: KIMMERLY, WILLIAM JOHN TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERWIDIS NUCLEIC ACIDS AND PROTEINS FILE PEPEPENCE. BILLAGORICE
& 8		CURRENT APPLICATION NUMBER: US/09/710,279 CURRENT FILING DATE: 2000-11-09 PRIOR APPLICATION NUMBER: 60/164,258 PRIOR FILING DATE: 1999-11-09
& 4	64 LeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlylleAla 83	; NUMBER OF SEQ ID NOS: 4472 ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 3564 ; LENCTH: 3618
که م	84 Aspaspasnlys	DNA ISM: Artificia RE: INFORMATION:
장 옵	98LysileGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGlu 115 1034 GAATTTAAAGATGATAAATAATAATACTGAAATTTAAAGAACTGAAATTTAAAGAATTAAAAGAATTTAAAAAAAA	INFORMATION: nucleic acid sequence 279-3564
ර යි		SCOTEB: 1.52e-23 296.50 nllarity: 47.54%
ठे ह	15	: 28.42% Mismatches: 17.54% Indels: 4 Gaps:
3 8	AAGT	-10-724-972A
g q	12) ASINGTANDILLEABPALAPNELYBThrileSerLyBalaLeuGly 169 ::::: ::: 1211 GATGACAACTTAATTAAAGATATGAAAAAATACAGAAAATTTAGGGAAAATCTACGAT 1270	Qy 1 GlyValGluSerValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeu 20 ::::: 555 GGAGTTGCACATATGAAAAAAGAGTCTTATTTTTATTGTCTCTAGTTTTAGTTTTTA 614
송 음	170 LysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLysLyslleGluGluTyrLys 189 :::::	Qy 21 IleAlaThrAlaAlaCysGlyAsnAsnSerSerAsnSerSerLysGluSerSer 39
<i>₹</i> 8	190 LysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGly 209 ::: :: ::: 1331 GATAAAACTAAAGACTTTAATAAGAAAGTAATGTATTTATTGGTTAACGAAGGTGAA 1387	
Sp qg	210 LeuLeualahisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPhe 228	
oy Oy	229 LysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyr 248	V8ProValGly1leAla
S a	249 LeuGlnMetasnThrGluThrLeuSerGlnValAsnPro	LysAsnArgllelleLysProLeuArgAsp 97
& a	262 GluargMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu 281 ::: :::::: ::::: 1544 GATCGTGGTTGTAGGTGGTAAAGCAACAACAATTCAAGTT 1588	LyslleGlyLysTyThrSerValGlyThrArgLysGlnProAsnLeuGluGlu
දු දු	282 GluLygABpProValTrpLysLysLeuAsnAlaValLygAsnGlnArgValAspIleLeu 301 	116 IleSerLysbreuLyspreuLleIleAlaAspAsnAsnAgHisLysGlylle 134
ò	302 AspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGlu 321	135

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-----LysThrIleSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeu 178
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|CATCCATT-----TCTATGATATCGACAGCACACGCTTTATTGACAGCCTCACT 555
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                                    AsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGlu
                                                                                                          GluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSerPhe
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Patent No. 6703492
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMID
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
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Sequence 2690, Application US/09543681A

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: UDCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UDCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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        TTAGATGAATTTAAAAAAGCTGCACCAAAAGCTAAAGTT---GTATATGTAGGTACAAGT 1076
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GATGACAACTTAATTAAAGATATGAAAAATACAGAAAATTTAGGGAAAATCTACGAT 1136
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                                                                                    LysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLysLleGluGluTyrLys
                                                                                                                                       LysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGly
                                AsnGluAsnIle-----AspAlaPheLys-----ThrIleSerLysAlaLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GluGlyThrThrLysValPro
                                                                                      TYPE: DNA ORGANISM: Artificial Sequence PEATURE: ORGANISM: Artificial Sequence: Synthetic OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: nucleic acid sequence US-09-710-279-461
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Matches:
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Mismatches:
Indels:
Gaps:
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 1044
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	qq	760		CAAAAGCCCGCAT	GGTCAAAATATAAA	AAAAAGGTTAGCAAAAAGCCCGGCATGGTCAAAATATAAATAA
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	Ор	820		TATTTAGCTATG	::: GATCGTGGTTCAGT	 AATCCAGATGTTATTTTAGCTATGGATCGTGGTTCAGTTGTAGGTGGTAAAGCAACAACA 879
	ò	274		rLeuLysGluLeu	GluLygAspProVa	AsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaVal 293
	QQ	880	0 AAT	CAAGTT	TTAAAAAACAAAGT	
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	gg	7.7		ACTATCAAACAA	ATTGATGAATTAAA1	FGAA 1020
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	US-10-724-	9722	-724-972A-6352 (1-335)) x US-09-710	-279-1267 (1	-1044)
	ò	16		LeuLeuPheValLeuIleAlaThrAlaAl	ılaAlaÇyşGlyAşn	ysGlyAsnAsnSerSerAsnSerSer 35
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	٥٨	36	LysGlu	SerSerL	00	IleLysHisGlu 48
	ДD	85		 AATAGTGATTCTA	::: AAGAAACTGTAACC	::: TCGAAAAAGAAAATAGTGATTCTAAAGAAACTGTAACCATCAAAAATAGTTTTGAAGCA 144
_	٥٨	49				-GluGlyThrThrLysValPro 55
	Dp 1	145		AATAATGGCAGTG	ataagaaaaaatc	
	٥٨	26	LysHisPr	ArgValValValL	euGluTyrSerPhe	oLysArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeu 75
	CP QC	205		AATGCCGTTGTAT	AAGAATCCTAAAAATGCCGTTGTATTAGATTATGGAGCGCTTGATGTTG	::: CTTGATGTGTTG 255
_	ò	9/		AspvalLysProvalGlyIleAlaAspAspAsnLys	.spAspAsnLys	

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Genuence 2208, Application US/09902540

j Sequence 2208, Application US/09902540

j Patent No. 6833447

genuence 2208, Application US/09902540

j Patent No. 683347

j APPLICANT: Goldman, Barry S.

j APPLICANT: Slater, Steven C.

j APPLICANT: Slater, Steven C.

j APPLICANT: Magand, Roger C.

j TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

j TITLE OF INVENTION: Myxococcus

j CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2000-07-10

j PRIOR FILING DATE: 2000-07-10

j PRIOR FILING DATE: 2000-07-10

j NUMBER OF SEQ ID NOS: 16825

j SEQ ID NO 2208

LENGTH: 702
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                                                       -----AAAGAATTAGGTGTGGCTGATAAAGTAAAAGGTTTACCTAAAAGGTGAAAATAAC 309
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                                                                                                                                                                              APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Wixxococus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(15849)
                                                                                                                                                                                                                                                                                                                                      ValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeu
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Setent No. 683447
Patent INFORMATION:
APPLICANT: Goldman, Barry S.
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, ORGANISM: Myxococcus xanthus US-09-902-540-2208
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---AAGGATGATTTTGCTGAAATGAATGCAACAAAAAAGAACGCATTCCGGCAATGGACGC 496
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497 GATCAGCTATTTTACTTCTTTATGAAACGGGAGACGGTGAAGCAAAAAGCTTGAAAAA 556
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Matches:
Conservative:
Mismatches:
Indels:
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; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1583
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1583
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
UNMERR OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 GTTTCAATGATGGGACTGTTAATGTTA-----AGTGCTTGTCAAACAAATAAA
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                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDGS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,035 FILING DATE: CLASSIFICATION SATE: RESIDENTION: PRIOR APPLICATION NUMBER: FILING DATE: FILING DATE: ATTORNEY/AGENT INFORMATION: ANAMER: ATTORNEY/AGENT INFORMATION: NUMBER: ATTORNEY/AGENT INFORMATION:
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Mismatches:
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Matches:
                                                                               ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9B369P2
RELEPRENCE/DOCKET NUMBER: 9B369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INPORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDENESS: double
JOPOLOGY: linear
US-09-071-035-37
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| Sequence 937, Application US/09134000C
| Sequence 937, Application US/09134000C
| Patent No. 661716.
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
| CURRENT APPLICATION NUMBER: US/09/134,000C
| CURRENT PILING DATE: 1990-08-13
| PRIOR PILING DATE: 1997-08-15
| NUMBER OF SEQ ID NOS: 6812
| SEQ ID NO 937
| LENGTH: 984
                                                                                                                                                                                                                                                                                                                              ArgValAspileLeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGlu 316
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                                                                                                                                                                                        PheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAsp------ValThr 237
                                                                                                                                                                                                     ProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGln 221
                                                               LysThrileSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHis 181
                                                                                                                                                                                                                                                                                                                SerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGln
      ATT----TCTGGTCGTCAACAAGATTATCAAGAACAATTAAAAGCCATTGCGCCAACCATT
                          GluLeu------LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPhe
                                                                                  GGCACTATT------TTTGATAAAGAAGAGTAGCTAAAGAAAAAATAACTGGCTTA
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                                                                              AAT------ATCCCTGCGTATTTGAAAAATACCAAAAAGTTGAATCAGCA 321
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499 GGCACTATT-----TTTGATAAGAAGGAGGTAGCTAAAGAAAAATAACTGGCTTA
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OY 238 LysGlyLeuSerLysTyrLeu	arysgluteuvalglu 324 ::: AATTGAAGCGTGCAA 966	; TITLE OF INVENTION: NATURAL PROMOTERS FOR GENE EXPRESSION IN BACILLUS SPECIES ; FILE REPERENCE: CLI686 US NA ; CURRENT APPLICATION NUMBER: US/09/891,641 ; CURRENT FILING DATE: 2001-06-26 ; NUMBER OF SEQ ID NOS: 81 ; SOFTWARE: Microsoft 97 ; SEQ ID NO 16 ; LENGTH: 954 ; TYPE: DNA ; ORGANISM: Bacillus subtilis US-09-891-641-16	Alignment Scores: Alignment Scores: Preda No.: 276.50 Matches: Bercent Similarity: Best Local Similarity: 16.36\$ Mismatches: 16.36\$ Mismatches: 12 US-10-724-972A-6352 (1-335) x US-09-891-641-16 (1-954) QY 9 LysIleLeuServalIleGlyLeuLeuPhevalLeuIleAlaThrAlaAlaCysGlyAsn 28 7 AAGATATCTTTACTTATTATTATTATTATTATTATTATTATTA	9y 29 AsnSerSerSerSerBerserLys
PPLICANT: GARY BRETT ITLE OF INVENTION: 1 ILE REFERENCE: 2709 URRENT APPLICATION DATE: RIOR APPLICATION NUM ANGEN OF SEQ ID NOS. Q ID NO 1393 UND NO 1393 TYPE: DNA DRGANISM: Proceus mi 9-543-681A-1393	Pred. No.: 2.49e-22 Length: 978 Score: 278.50 Matches: 94 Pred. Score: 17.84 Matches: 94 Percent Similarity: 17.34 Mismatches: 132 Mismatches: 132 Mismatches: 132 Mismatches: 145 Mismatches: 145 Mismatches: 15.484 Mismatches: 16.484 Mismatches: 16.484 Mismatches: 16.484 Mismatches: 17.895 Mismatches: 18.455 Mismatches: 19.455 Mismatches: 19.456 Mismatches: 19.456	Qy 29 AsnSerSer		430 159 490 178 550 550 607 607

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GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsp 299
                                                                                                                                                                                                                                                                                ATCAGAATCAGACAAGGCAACATTTACCTCTGAACAGGTGTATTTCAACTCCACA 645
                                                                                                                                                                                                                                                                                                             Leu---SerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSer 241
                                                                                                                                                                                                                                                                                                                                                                         LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro 261
                                                                                                                                                                                                                                                                                                                                                                                            Gluargmet Phelle---Met ThrasnLysalaSerSerAsnGlupro---SerLeulys 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 AlavalAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe 222
                                                                                             465
                                                                                                                                                ThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              grcaactcagreeaccrcrcecacaagecegcacagcrreeaagecacaaagreedr
                                                                                                                                                                                                                                                                                                                                            CTATACGGTGATTTAGGCCTTAAG-----GCGCCGAACGAAGTAAAGGCTGCAAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11eLeuAspArgAsp------gevTrpAlaArgSerArgGlyLeu
                                                                                            ACGATCCCAGTTTCTCATATCTCTTCAAACTGGAAAGGAAACATG------ATGCTT
                                                                                                                         IleSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLys
                                                                                                                                                                                       LysileGluGjuTyrLygLysGlujleThr---MetAspLysAsnGlnLygValLeuPro
ilelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaPro
                             355 ATCCTTGCTTCAACAAAGTTTCCGGAAAAAACGCTGCAAAAAATCAGCACAGCAGGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application US/09071035
Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 IleSerSerGluGlu 317
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-071-035-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 ArgLeuGluGluHisAspLysLleGluGluTyrLygLysGluIleThrMetAspLys 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlylleAlaAspAspAsnLysLysAsnArglleileLysProLeuArgAspLysIleGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 ileAlaProThrileGluLeu------LysSerPheAspGlyAspTyrAsnGlu 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 ATTGCGCCAACCATTTACTTAGCTGTAGATGCCAAAAATCCTTGGGCATCAACGAAACAA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnijeAspAlaPheLysThrijeSerLysAlaLeuGlyLysGjuGluGluGlyLysLys 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CysGlyAsnAsn-----SerSerAsnSerSerLysGluSerSerLysAspGly 42
                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspVal-----LysProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 GCTGCGCCAACTAAAAAT-------ATCCCTGCGTATTTGAAAAATACCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLys
                                                                                                                                                                                                                                                                                                                                                           43 ValGlulleLysHisGluGluGluGlyThrThrLysValProLysHisProLysArgValVal
                                                                                                                                                                                                               889
96
1129
129
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Mismatches:
Indels:
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                                                                                                                                                                                                                  Length:
Matches:
                                PB369P2
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB365
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                               3.47e-21
268.00
47.32%
30.28%
15.86%
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Best Local Similarity:
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US-09-071-035-39
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Query Match:
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659 TACGAATATGTTTTAGAAAAAATCCTGGGATTCTCTTTGTGGTAGATCGCACAAAGCA 718
                                                                     SerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsn 291
                                                                                                       119 ATTGGTGGCGACGATTCAAAAGATAACGTGCGCTGCAAACGAATTGATTCAAAAAACCGAT 778
                                                                                                                                                                                    311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kongelus, Mark APPLICANT: Kongelus, Mark APPLICANT: Sch"der, Hartwig APPLICANTON: TRANSCOFT TITLE OF INVERTION: TRANSCOFT TITLE OF INVERTION: TRANSCOFT TITLE OF INVERTION: TRANSCOFT TOOL 06-29/602,787A

PRIOR PRILICANTON WOMER: US/99/602,88 60/141031

PRIOR APPLICANTON WOMER: D999/01-28

PRIOR APPLICANTON WOMER: D999/01-28

PRIOR PRICATION WOMER: D999/01-28

PRIOR FILING DATE: 1999/01-28

PRIOR FILING DATE: 1999/01-28

PRIOR FILING DATE: 1999/01-29

PRIOR PELING DATE: 1999/01-29

PRIOR FILING DATE: 1999/01-29

PRIOR PELING DATE: 1999/01-29
                                                                                                                                                                                                 AlaValiyeAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly
                                                                                                                                                                                                                                                       312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
                                                                                                                                                                                                                                                                                               Sequence 571, Application US/09602787A Patent No. 6696561 GENERAL INFORMATION:
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APPLICANT: Kr"ger, Burkh
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191 GAAGCATCCACCAGCTCTGCGACTCGC-----GAATTCACAGACGCTCACGGAACAACC 244
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940765.7
PRIOR APPLICATION NUMBER: DE 19940766.5
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PRILING DATE: 1999-08-27
PRIOR PRILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR PRILING DATE: 1999-08-27
PRIOR PRILING DATE: 1999-08-37
PRIOR PLILING DATE: 1999-08-37
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR PLILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942077.7
PRIOR APPLICATION NUMBER: DE 19942079.3
PRIOR PLILING DATE: 1999-09-03
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ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.48e-21
266.00
44.79%
25.87%
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OTHER INFORMATION: RXN03084
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 571
LENGTH: 1041
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23390 GCCGCCGCGTCCACCTCCCGCCGGAGGCCCGGAGGCCCGGACGGTCCAC 23331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 LysasnargileileLysProLeuargaspLysileGlyLysTyrThrSerValGlyThr 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 ArglysGlnproAsnLeuGluGluIleSerLysLeulysProAspLeulleIleAlaAsp 127
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                                           300 ileleudspargaspleuTrpalaargserargGlyleulleserSerGluGluMetAla 319
                                                                       73 ATTTTAGACCGTGACTTATGGGCAAGATCACGTGGTTTAATTTTCTTCAGAAGAAATGGCA 132
               72
                                                                                                                                                                                                                                                            APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Misgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1250
LENGTH: 28194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 PheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLys
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23210 CCCCAGCACCTGACCGGG----TTCCGGGAC-----GCGAAGTACCCGCGCGCATGGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeulyslleLeuServallleGlyLeuLeuPhevalLeulleAlaThrAlaAlaCysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis
33 CAGATTAGAAAAAGACCTGTATGGAAGAAATTAAACGGTGTGAAAAATCAACGTGTTGAT
                                                                                                          320 LygGluLeuValGluLeuSerLysLysAspSerLysLysLysAspAsnLys 335
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Matches:
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                                                                                                                                                                                                  Sequence 1250, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
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257.00
50.16%
25.71%
15.21%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 GluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsp 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 ValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAspLeu 305
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                                                                                                                                                                                           ThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAla 212
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                                                                                                                                                                                                                                                      HisproSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeu 232
                                                                                                                                                                                                                                                                                                                SerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsn 252
                                                                                                                                                                                                                                                                                                                                               CICACCATTCCTGATCGAATGGAAG 781
                                                                                                                                 GluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIle 192
            GlylleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysSerPheAspGly 152
                                                                      153 AspTyrAsnGluAsnIleAspAlaPheLysThrileSerLysAlaLeuGlyLysGluGlu 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   590 GAATCCGAGGATCTCATCCAGGCTTTAATGACAAGTGCGAAGAGATCAAGTCCGAGGAT
                                306 TrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeu 322
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265.00
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Best Local Similarity:
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US-09-134-001C-2023
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Db 88 AATGAAGAAAATACTICTAAAGAGCATGCGCCTGATAAATAAATTAAAT	69	70	 ATTACGGTGTA	268 ACTGCTGATAAAGGAGTTTTACCATGGACAGAAAA	Oy 102 TyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysPro 121	Qy 122 AspLeullelleAlaAspAsnAsnArgHisLysGlyllefyrLysAsp 137	Db 388 GATGTTATCTAGCAGGTTATTCTGGTATAACTAAAGAAGATTATGACACT 438 Qy 138 LeuasniyslealaaprothrileGluLeuivsserPheasnglyaantvrasngluben 157		OY 158 IleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGluGlyCr 174 DD 199GATATGATTAAAATTCAAAAGCCTTAGGTAAGAAAAAAAA	i		QY 187 GlufyrLysLysLysLyslulleThrMetAspLysAsnGlnLysValLeuProAlaVal 204 Db 604 GAAATCAAAGGAAAAAQTATATTACTATGATTAAT	0 7		lAsnPro : AAATGAT	QY 262 GluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu 281				ម	; STATE: Maryland ; COUNTRY: USA
GCTAGCCAGC	22982 GTCTTTGGCAAGGAGAGAGCGCGCGCGCCTGATTGAGACCTGCGCAAGTCGCTGGCG	22		227	_မ္ပ _မ္ပ	22	Oy 267 MetThrasnLysalaSerSerAsnGluProSerLeuLysGluLeuGluLysAsp 284 ::: :::::: Db 22709 ATCGACCGGGAACGCCACTGACTGATCGAAACAAAAAAAA	Oy 285 ProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsplleLeuAspArgAsp 304	δ,	22	SULT 29	US-09-583-110-1062 ; Sequence 1062, Application US/09583110 ; Patent No. 6699703 ; GENERAL INFORMATION:	<pre>// APPLICANT: Lynn Doucette-Stamm et al. // TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus // TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics // FILE REFERENCE: PATH00-07A</pre>	; CURRENT APPLICATION NUMBER: US/09/583,110 ; CURRENT FILING DATE: 2000-05-26 ; PRIOR APPLICATION NUMBER: US 09/107,433 ; PRIOR FILING DATE: 1998-06-30	FRIOR APPLICATION NUMBER: US 60/085,131 PRIOR FILING DATE: 1995-05-12 PRIOR APPLICATION NUMBER: US 60/051,553 PRIOR FILING DATE: 1997-07-02	SEQ ID NOS: 5322 SEQ ID NOS: 5322 SEQ ID NOS: 5322 SEQ ID NO 1062 SEQ ID NO 1062	 GRGANISM: Streptococcus pneumoniae US-09-583-110-1062 Alignment Scores) <u>5</u> _5	US-10-724-972A-6352 (1-335) x US-09-583-110-1062 (1-1035)	Oy 13 ValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAenAsnSer 30 ::: ::: ::: ::: Db 28 CTAATAGCTATTTTAGCTATATTTTAGCGCTTGTTCTTCTAATTCTGTTAAA 87	Oy 31SerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGluGlu 49

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4.6e-19
250.00
46.45%
27.22%
14.79%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------LeuhrgAspLysIleGlyLysTyrThrServalGlyThrArgLysGln 110
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117
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Brookes, A. Anders
REGISTRATION UNMERS: 36.373
REFERENCE/DOCKET NUMBER: PB340P1
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
IELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 164: SEQUENCE CHARACTERISTICS: LENGTH: 9707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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46.18%
26.76%
14.97%
                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                     272 ---SerSerAsnGluProSerLeuLysGlu-----LeuGluLysAspProValTrpLys 288
                                                                                                                                                                                                                                                                                  289 LysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArg 308
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----LysLysGluIleThrMetAspLysAsnGlnLys 199
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                                                                                                                                                                                                                                                     309 SerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLyB
                                                                                             220 GlyGlnPheLeuSerGln---LeuGlyPheLys-----GluAlaLeuSerAspAspVal
                                                                                                                                          237 ThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeu
                                              200 ValleuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrVal
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Matches:
Conservative:
Mismatches:
                                                                       5360 AAAATGGCAĞCCTTTGGTĞCCAAAİCTCGTTTC--
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ADDRESSEE: GENOWE THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham STATE: Massachusetts COUNTRY: USA COUNTRY: USA COUNTRY: USA MEDIUM TYPE: CD/ROM ISO9660 COMPUTER: <unknown> OPERATING SYSTEM: <unknown> SOFTWARE: <unknown></unknown></unknown></unknown>	CURRENT APPLICATION DATA: CURRENT APPLICATION NUMBER: US/09/107,433 FILING DATE: 30-70n-1998 FILING DATE: 30-70n-1998 FILING DATE: MAPPLICATION NUMBER: 60/05153 FILING DATE: MAY 12, 1997 ATTORNEY/AGENT INFORMATION: MAME: Ariniello, Pamela Deneke REGISTRATION UNMBER: GTC-011 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:	INFORMATION FOR SEQ. 1D NO: 2206: SEQUENCE CHARACTERISTICS: LENGTH: 978 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Streptococcus pneumoniae FEATURE: NOMENCEY: misc_feature	SEQUENCE DESCRIPTION: SEQ ID NO: 2206: US-09-107-433-2206	Qy 20 LeulleAlaThrAlaAlaCysGlyAsnAsnSerSerSerAsnSerSerLysGluSerSer 39
Db 109 TCTGCTCCAACAGAGGTAACCATTAAAAGTTCACTGGACGAGGTCAAACTTTCCAAAGTT 168 Qy	Db 262 GTTCCGACTTATCTAAAAGACCTAGGGAACTGTCAAAAATGTTGGTTTTATGAAAGAA 321 Qy 111 ProAshLeugluglulleSerLysleuLysProAspLeulElleAlaAspAsnAsnarg 130 Db 322 CCTGATTTAGAAGCTATCGCCGCCTTGATCTATTATGATTATCGCTTCACCAGTACA 381 Qy 131 HisLysGly1leTytLysAspLeuAshLyslalaAtTATTAGTTATCACCAGTACA 381 Db 382 CAAAAATTCGTAGACAATTCAAAGAAATCGCCCCAACCGTTCTCTCCAAGCAAGC 438 Qy 151 AspGlyAspTytAsnGluAsn1leAspAlaPheLysThrIleSerLysAlaLeuGly 169 439 AAGGACGACTACTACCAAGGCTAATATCGAATCCTTAGCAAGGCTTCGGC 498	170 499 188 559 200 619 220	0.52	Trpalaargserarg

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CTHER INFORMATION: RXN00466
US-09-602-787A-597
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APPLICANT: Sch"der, Hartwig
APPLICANT: Lalder, OBKAR
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYEBBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
FILE OF INVENTION: TRANSPORT
FILE OF INVENTION: DG-23
CURRENT PILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-08
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PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 VallanproGluargMetPhelleMetThrasnLysAla-------Ser 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAsnGluProSerLeuLysGlu-----LeuGluLysAspProValTrpLysLysLeu 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 GlyGlnPheteuSerGln---LeuGlyPhetyaGluAlaLeuSerAspAapValThrLys 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        664 ---rcriticitigraccaaaccitigaaatitcaaacr-------Gatacaacrr 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 GlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGln 258
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511 GAAACTGGTACACAGAAAAAGAATTGGCCAAGCTAGACAAGAGCATCCAAGAA 570
                                                                                                                                                                                                                                                                                                                                           571 GTCGCTACTAAAAATGAAAAGGCCCTTGCGATCCTCCTTAATGAAGGA 630
                                                                                                                                                                                                                                                                                                                                                                                                                            200 ValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrVal 219
                                                                                                                                                                     .51 AspGlyAspTyrAsnGluAsnIleAspAla---PheLysThrIleSerLysAlaLeuGly 169
                                                                                                                                                                                                                                                       170 Lys-----GluGluGluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGlu 187
ProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsnArg 130
                                                                                 131 HistysGlylleTyrLysAspLeuAsnLysileAlaProThrileGluLeuLysSerPhe 150
                                                                                                         311 GlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          820 AGCAACAACGGTGTCCTAGAAATGCCCTTATCGCTGAAACACCT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 597, Application US/09602787A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Pompejus, Mark
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PRIOR APPLICATION NUMBER: DE 19932212.0
PRIOR PELLING DATE: 1999-07-09
PRIOR PELLING DATE: 1999-07-14
PRIOR PELLING DATE: 1999-07-14
PRIOR PELLING DATE: 1999-07-14
PRIOR PELLING DATE: 1999-07-14
PRIOR PELLING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR PELLING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR PELLING DATE: 1999-08-27
PRIOR PELLING DATE: 1999-08-27
PRIOR PELLING DATE: 1999-08-27
PRIOR PELLING DATE: 1999-08-27
PRIOR PELLING DATE: 1999-08-31
PRIOR PELLING DATE: 1999-09-03
FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932125.6
FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932128.0
FILING DATE: 1999-07-09 FILING DATE: 1999-07-09
PILING DATE: 1999-07-09
PILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932191-4 FILING DATE: 1999-07-09 APPLICATION NUMBER: DE 19932209.0 FILING DATE: 1999-07-09 APPLICATION NUMBER: DE 19932180.9 FILING DATE: 1999-07-09 APPLICATION NUMBER: DE 19932182.5 DE 19932124.8 TYPE: DNA ORGANISM: Corynebacterium glutamicum

Pred. No.	.: 1.11e-18 Length:	, 40£	Troalabrook
Score: Percent	247.50 Matches:	0 0 0	epatant
Best Local	Similarity: 26.76% Mismatches:	Db 1010 -	/D
Ouery m	••	. Qy 316 G	GluGluMetA
US-10-7	-597 (1-1)	Db 1061 G	GAACATCTCG
ò	9 LysileLeuServalileGlyLeuLeuPheyalLeulleAlaThrAlaAlaCys 26	RESULT 34 US-09-328-352-318	18
QQ		; Sequence 318, ; Patent No. 65	Applicat:
ò	27 GlyAsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGly 42	GENERAL INFOR	MATION:
QQ	176 TCTAACAATGCAGATGACACCGACGCTGATTCAACATCCACGGGAAACTCCGCTTTTCCT 235	; TITLE OF INVENTION: NO.	ENTION: NI
'n	43 ValGlulleLy8HisGluGluGlyThrThrLysValProLysHisProLysArgValVal 62	; FILE REFERENCE: GTC99-	CE: GTC99
QQ Q	236 GTTTCGATTGAACACGAGTTCGGAACCACCACAATCGATGATGTACCCGAAAGAGTTGTC 295	; CURRENT FILING DATE: ; NUMBER OF SEQ ID NOS:	NG DATE:
ò	63 ValLeuGluTyrSerPheValAspAlaLeuValAjaLeuAspValLy8ProValGjylle 82	; SEQ ID NO 318 ; LENGTH: 975	
q	296 ACCCTTGGCGTTACCGACGCCGATATTGTCCTCGCATTGGGGACCGTCCCAGTAGGCAAC 355	; TYPE: DNA ; ORGANISM: Acinetobact	cinetobac
ò	83 AlaAspAspAsnLysLysAsnArgllelleLysProLeuArgAspLysIleGly 100	US-09-328-352-3	81
. q ₀	356 ACCGGATACAAATTCTTCGAAAACGGATTGGGACCGTGGACTGATGAGTTAGTGGAAGGC 415	Alignment Scores Pred. No.:	
ò	101 LysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGlulleSerLysLeu 119	Score: Percent Similarity:	LEY:
q	416 AAAGAATTAACACTGCTTGACTCTGATTCCACACCAGATCTTGAACAAGTAGCAGCCCTG 475	Best Local Simi Query Match:	larity:
ð i		DB: IIS-10-724-9728-6352	4
gg (GAGCCAGACCT	7 14 T	
È t		3.4	
2 ;	ICIGALAI	34	SerSerIvaG
s ස	158 ILEASpAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGlyLysLysLysArg 177	9 6	ACCACTCAAGC
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જે દ	ysGlulleThrMetAspLysAsn 	154	inflysvalpri ::: ACGGTGATAGA
a :			o Telala Vita I
· 참 옵	198 GInLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisPro 214	214	Leuvainiale CTAGATCAACT
ò	SerAsnSer	. Qy 92 II	IleLysProLe
qa	AAATACGGTGCCTGCCGGGGGATGCACGGGGAATTCCTCGATTCATTGGCATT	Db 274 GP	 Gaaaaatataa
ò		Qy 112 AE	AsnLeuGluGlu
qq		Db 328 AA	AATATGGAAAG
ò	roGluArqMetPhe	Qy 132 Ly	LysGly1leTy
qq		Db 385 GT	GTTAATCAGTA'
ò		Qy 152 GI	GlyAspTyrAsı
අු		Db 436 AT	ATTAACTTCAAG
ò	286 ValTrpLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAspLeu 305		IleSerLysAla
qa		Db 4,96 TT	TTAGGAAAATI
		Qy 1,84 Ly	le4 LysIleGluGlı

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reton et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
9-03PA
NUMBER: US/09/328,352
11999-06-04
: 8252
                ----SerSer 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roLysHisProLysArgValValValLeuGluTyrSerPheValAspAla 71
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TCAATGTCCCGATTATGGGAATGCCAAAAGATTATGTTCCACACTTTTTG 273
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|ACAATAGCGAGAGTAATCATATTGGTCTGGTTAAAGACCATATGATGACC 495
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                                                                           AlaLysGluLeuValGluLeuSerLysLysAspSer 330
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77
135
38
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
SerArgGlyLeuIle------
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Sequence 69, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 ProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsn 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 GlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSer 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 SerGlnLeuGlyPheLysGluAla-----LeuSerAspAspValThrLysGlyLeuSer 241
                                                                                                                                                                                                                                                                              LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro 261
                                                                                                                                                                                                                                                                                                              .::::::||| ::: :::||| ::: :::||| ... :::||| ... ::: ||| | ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::|| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||| ... :::||
CAAGTGAAGCAAGTA---CAAGCCGTAACGGCCAATGGCCCAGAAAGAGCATTAGTCGTT
                                                                                                              :::
613 CTTCATAACAATGGGGCATTTAGTAATTTTGGTATTCAGTCACGCTATGGCTTTATTTTT
                                                                                                                                                                                                            ValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 GluGluMetAlaLysGluLeuValGlu 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P8369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPRAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-071-035-69
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US-09-071-035-69
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229 LysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyr 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCAAAAAC------GGCGAAAATGTCACCTGGCGTGATCAATTGGAAGAT 477
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                                                                                                                                                                                                                                                                                                                                                                                       ------GTCCCACTATTTCC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----cardaagraacagaracctraggcaaraaagraaccdrccccgaaacccaaa 180
                                                                                                                                                                                                                                                                                              IleLysHisGluGluGluGlyThrThr------LysValProLysHisProLys 59
                                                                                                                                                                                                                                                                                                                                                              Argvalvalval-----LeuGluTyrSerPhevalAspAlaLeuvalAlaLeuAspVal 77
                                                                                                                                                             25
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679 CAA-----GTICCAAAATTAGIGGAAGAAATTCTAAAAAACGCTACTGCGGATIGG
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TTAAAAAAGACGGTCCTAATTGGTACAACCCTTCTTGGTTCATTCTTACTCGCAGCT
          954
64
103
20
                                                                                                                               (1-335) x US-09-071-035-69 (1-954)
            Length:
Matches:
Conservative:
Mismatches:
Indels:
          6.36e-18
240.00
45.28%
27.50%
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                                        Percent Similarity:
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Query Match:
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Alignment Scores:
Pred. No.:
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0y 204 valAiaAlaiyaSerGiyLeuLeuAlaHisProSerManSaTyTvalGiyGilahBiateu 223 646 CTCCTCACCGGGGCCCCTATGGCCCCTATGGCCCCTATGGCCCTCATGGCCCCATGGGGGGGG	TOPOLOGY: linear US-08-961-083-23 Alignment Scores: 1.66e-17 Length: 895 Score: 236.00 Matches: 88
00 239 Lyeleuwanialavallypakanolinkgy(alaspileteukaphygaspleurTrahlakig 308 232 Aurill	184 184 412

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863 CTCATGATTGAAGACATACAAAAAGCTTTGAAA 895
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       relephone: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 895 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
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236.00
46.22%
26.59%
13.96%
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                                                                                                                                   CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                          Ala---PheLysThrIleSerLysAlaLeuGlyLys-----GluGluGluGlyLysLys 176
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GAAAAAATATGTGGGAATGCCTACAAAAGTGTTCCGACTTATCTAAAAGACCTAGTG 220
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                                                                                                                                                           SerphevalaspalaLeuvalalaLeuAspvalLysProvalGlyIleAlaAspAspAsn 86
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                                                                                          47 HisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyr
                                                                             AsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGlu-----1leLys
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         Conservative:
Mismatches:
Indels:
Gaps:
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GAAAAAATTGTCGGAATGCCTACAAAACTGTTCCGACTTATCTAAAAAAAGACCTAGTG 220
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RESUL: 30
US-09-536-784-23
i Sequence 23, Application US/09536784
j Sequence 23, Application US/09536784
j Sequence 23, Application US/09536784
j GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
CORRESPONDENCE ADDRESS: 452
j CORRESPONDENCE ADDRESS:
STREET: 9410 Key West Avenue
TITLE OF INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 AsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGlu-----ileLys
                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: CURNOWN>
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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ò	120 Lyapro	Application of the form	1 SAMASAMACA16		280	Score: Percent	Similarity.
q		GAGCCTGATTTGATTATCGCTTCGCCACCAAAAAAAAAA		spieuAsn	6 F	Best Local S Query Match:	Best Local Similarity Query Match:
ò	140 LVBIL	AlabroThrileGluicut		Trcaaa	337	DB:	
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; A		GCTABATATCCATASCATASATALCUGIYLYS-	areuglybys	GluGluGluGlyLysLys	176	අු	31 GCGGCTTC
}		al ceral colladoragio	CCTTCGGCGAAAC		457	δ	43 ValGluIl
Š 6		ArgleuGluGluHisAspLysLysIleGluGluTyr-	eG uG uTyr :::	ArgLeucludiuHisAspLysLyslugluGluTyr	188	qq	62
g d		ACCAAGCTAGACAAGAGCA	rccaagaagrege		517	ò	58 ProLysAr
ò 1		<pre>3lulleThrMetAspLysAs</pre>	snGlnLysValLe		208	QQ	 127 CCCAAACG
Q Q		SCCCTTGCGATCCTCCTTÀ	TGAAGGAAAAT		577	ò	76 AspValLy
<i>ह</i> े ∶		euAlaHisProSerAsnSe	erTyrValGlyGl	GlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGly 22	227	Dp	 175 GGAGAAAA
g G		1	OLL	TCTTTCTTGTACCAAACCTTGAAA 607	70	ò	93 LysProLe
8 1		GluAlaLeuSerAg	PASDValThrLy	GluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLys 245		q	 235 AAAGAATT
Q C	608 TTCAAAC	TTCAAACCAACTGATACAAATTTGAAĠAĊTCACGCCACĠĠA-	AGACTCACGCCA	ACGGA 649	. 61	ò	113 Leu
ò		YrLeuGlnMetAsnThrG]	uThrLeuSerGl	GlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe 265	55	q	259 ATTTCCTA
ପ	650	CAAGAAGTCAGCTTTGA	AAGTGTCAAAGA	-CAAGAAGTCAGCTTTGAAGTGTCAAAGAAATCAACCCTGACATCCTCTTT 700	<u> </u>	ò	127 AspAsnAs
ò		IleMetThrAsnLysAla	Se:	SerSerAsnGluProSerLeuLys 279		ΩÞ	
q	701 GTCATCA	ACCGTACCCTTGCCATCGG	TGGGGACAACTC	GTCATCAACCGTACCCTTGCCATGGGGGGGACAACTCTAGCAACGACGGTGTCCTAGAA 760	0	ò	145 IleGluLe
Š	280 Glu	LeuGluLysAspProVa	lTrpLysLysLeı	LeuGluLysAaspProValTrpLysLysLeuAsnAjaValLysAsnGlnArg 297	-	qq	379 TATGTAGT
ορ	761 AATGCCC	AATGCCCTTATCGCTGAAACACCT		GCTGCTAAAATGGTAAG 802		ò	
È	298 ValAspi	leLeuAspArgAspLeuTr	pAlaArgSerArc	ValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGlu 317	7	; A	
d d	803 ATTATCC	AACTAACACCAGACCTCTG	 GTATCTAAGCGG	ATTATCCAACTAACACCAGACCTCTGGTATCTAAGCGGAGGGGGGACTTGAATCAACAAAA 862		ò	
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RESULT US-09-1	RESULT 39 US-09-134-000C-2609				_	; <u>8</u>	
Seque	nce 2609, Appli	cation US/09134000	r)			ò	217 SerTvrVal
GENER	AL INFORMATION:	TOOTTOOLS OF TOO				, 4 <u>0</u>	
; TITE	E OF INVENTION:	NUCLEIC ACID AND I	AMINO ACID SE	TITLE OF INVENTION: NUCLEIC AND AMINO ACID SEQUENCES RELATING TO		<i>\</i> 0	
; FILE ; CURR	REFERENCE: 032 ENT APPLICATION	032796-032 TION NUMBER: US/09/134	2000	ACTION AND INERAPEUTICS		අු	625 GGCCTCCAA
; CURR ; PRIO	ENT FILING DATE R APPLICATION N	CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778			<u></u>	ò	247 ProTyrLeu
, NUMB	PRIOR FILING DATE: 1997-08 NUMBER OF SEQ ID NOS: 6812	1997-08-15)S: 6812				QQ	676 GATTGGAAT
SEQ I	SUFTWARE: PatentIn version SEQ ID NO 2609	version 3.1				ò	267 MetThrAsn
TYP	LENGTH: 906 TYPE: DNA	•			_	q	736 GTAAACAGC
US-09-1	8	Enterococcus faecalis -2609				ć	287 TrpLysLys
Alignme	Alignment Scores: Pred No.					qq	778 TGGAAGAAC
		1.7e-17 Le	Length:	906	_	δ	307 AlaArgSer

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Sequence 71, Application US/09071035

Patent No. 6448043

PATILE OF INVENTION:
TITLE OF INVENTION:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

ZIP: 20850
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: ASCII Text
CURRENT APPLICATION DATA:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
PATILE OF INFERENCE OF SCIENCES, INC.
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
PATILE OF INFERENCE OF SCIENCES, INC.
SOFTWARE: US/09/071,035
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|CGGATTATTGCGAGTTATTAGAA------GATTATCTAGTTGCATTAGGAGAA 145
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26 CysGlyAsn---AsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGlu
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Gaps:
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TELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 868 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 -------GluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsn 128
                                                                                                                                          129 AsnArg-----HisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGlu 146
                                                                                                                                                                                                                                                                              147 LeulysSerPheAspGlyAspTyrAsnGluAsnIle-----AspAlaPheLysThr 163
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350 GTCAAAAAC------GGGGAAAATGTCACCTGGCGTGATCAATTGGAAGAT 394
146 AAACCAGTGGCACAATGGACAGTTGGACAAGGCAGCATTCAAGATTATTTAGCGAAAGAA 205
                                     LeuArgAspLys1leGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeu--- 113
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Sequence 3782, Ap
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Sequence 2556, Application US/08956171E

Sequence 2556, Application US/08956171E

Setent No. 6593114

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCES: 5256

STREET: 9410 Key West Avenue

CITY: Rockville

STREET: Maryland
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                                                                                                                                                  305 LeutrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGlu 324
                                                                                                                                                                                  285 ProvaltrpLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAsp 304
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3782, Application US/09710279
| Sequence 3782, Application US/09710279
| Patent No. 6703492
| GENERAL INFORMATION:
| APPLICANT: KIMMERLY, WILLIAM JOHN
| TITLE OF INVEWTION:
| FILE REFERENCE: PUJ480US
| FILE REFERENCE: PUJ480US
| CURRENT APPLICATION NUMBER: US/09/710,279
| CURRENT FILING DATE: 2000-11-09
| PRIOR APPLICATION NUMBER: 60/164,258
| PRIOR FILING DATE: 1999-11-09
| NUMBER OF SEQ ID NOS: 4472
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NOS: 3782
                                                                             28 CCTGTATGGAAGAAATTAAACGCTGTGAAAATCAACGTGTTGATATTTTAGACCGTGAC 87
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7 OTHER INFORMATION: Description of Artificial Sequence: synthetic
7 OTHER INFORMATION: nucleic acid sequence
1S-09-710-279-3782
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US-10-724-972A-6352 (1-335) x US-09-134-001C-2023 (1-183)
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity: 1
Query Match: 1
DB:
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US-08-956-171E-2556
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| Sequence 2023 Application US/09134001C
| Patent No. 6380370
| Patent No. 6380370
| Patent No. 6380370
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REPERENCE: GTC-007
| CURRENT PILING DATE: 1990-08-13
| PRIOR PPLICATION NUMBER: US 60/064,964
| PRIOR PPLICATION NUMBER: US 60/064,964
| PRIOR APPLICATION NUMBER: US 60/055,779
| PRIOR FILING DATE: 1997-11-08
| PRIOR FILING DATE: 1997-08-14
| NUMBER OF SEQ ID NOS: 5674
| SEQ ID NO 2023
| LENGTH: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15374, A Sequence 15910, A Sequence 12018, A Sequence 12018, A Sequence 16017, A Sequence 14712, A Sequence 16739, A Sequence 14917, A
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 4
US-08-781-986A-2556
is Sequence 2556, Application US/08781986A
is Sequence 2556, Application US/08781986A
is GENERAL INFORMATION:
APPLICANT: Charles Kunsch
it TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Rockville
CUNTRY: USA
ISTE DISKETTE, 13.50 inch, 1.4Mb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
COMPUTER: ASCII Text
CURRENT APPLICATION DATA:
HING DATE:
FILING DATE:
CURRENT APPLICATION NUMBER: US/08/781,986A
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COMPUTER READABLE FORM:

WEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION CURNOWN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/09,861
FILING DATE: January 5, 1996
FILING DATE: January 5, 1997
APPLICATION NUMBER: 06/781,986
FILING DATE: January 3, 1997
APPLICATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 46,789
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEG ID NO: 2556:
SEQUENCE CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
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RESULT 5
US-08-956-171E-355

US-08-956-171E-355

Sequence 355, Application US/08956171E

Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon
Craig A. Rosen

Steven C. Barsah

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 25.56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 TyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysPro 121
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ZIP: 20850

COMPUTER: USA

COMPUTER: READABLE PORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 5, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
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Matches:
Conservative:
Mismatches:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: BENBON, BOD
REFERENCE/DOCKET NUMBER: 30,446
REFERENCE/DOCKET NUMBER: 9B248PP
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2556:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: MUCHAEL CALL
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Alignment Scores:
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Pred. No.:
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Sequence 355, Application US/08781986A

Sequence 355, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
INUMBER OF SEQUENCES: 5555

CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 COPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A FILING DATE:
FILING DATE:
RAPPLICATION NUMBER:
ATRONARY/AGENT INFORMATION:
AND APPLICATION NUMBER:
FILING DATE:
ATRONARY/AGENT INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 355: US-08-956-171E-355
                                                                                                                                                                                                                                                                                                                                                        Gaps:
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REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-781-986A-355
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; Sequence 15, Application US/09830217
; Patent No. 6521441
; GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERRICE: PAGE/PCT
CURRENT FILING DATE: 2001-04-24
FRIOR APPLICATION NUMBER: US/09/830,217
CURRENT FILING DATE: 1999-04-01
; PRIOR PILING DATE: 1999-04-01
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: 1998-04-01
; RIOR APPLICATION NUMBER: 60/084,674
; PRIOR FILING DATE: 1998-04-01
; ROOFWARR: PATENTIN VOI: 2.0
; SEQ ID NO 15
; LEMETH VOI: 2.0
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; Sequence 15, Application US/10278946
; Patent No. 6821754
; GENERAL INFORMATION:
; APPLICAMY: Simpson et al.
; TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
; FILE REFERENCE: P8461USD1
; CURRENT APPLICATION NUMBER: US/10/278,946
; CURRENT PILING DATE: 2002-10-24
; PRIOR PILING DATE: 2001-04-24
; PRIOR PILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
; PRIOR FILING DATE: 1999-03-18
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Matches:
Conservative:
Mismatches:
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   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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; ORGANISM: Staphylococcus aureus
US-09-830-217-15
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Best Local Similarity:
Query Match:
DB:
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RESULT 10
US-08-781-986A-238

Sequence 238, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                                                                                                                                                      111 ProAsnLeuGluGluileSerLygLeuLysProAspLeulle 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 ProAsnLeuGluGluileSerLysLeuLysProAspLeuile 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/781,986A

FILING DATE:
CLASSIFICATION ATA:
APPLICATION NUMBER: BRICK APPLICATION BOD THE FILING DATE:
APPLICATION NUMBER: PR146

FILING DATE:
APPLICATION NUMBER: PB248PP
FELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8504

TELEPHONE: (301) 309-8512

INFORMATION FOR SEQ ID NO: 238:
LENGTH.
                                                                 3775
14
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                                                                                                                                                                      US-10-724-972A-6352 (1-335) x US-08-956-171E-238 (1-3775)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
; SEQUENCE DESCRIPTION: SEQ ID NO: 238:
US-08-956-171E-238
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STRANDEDNESS: double
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
                                               Alignment Scores:
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US-09-949-016-14517/c
; Sequence 14517, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: 60/241,755
    PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
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; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
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105-09-949-016-14516/C

15 Gequence 14516, Application US/09949016

15 Patent No. 6812339

15 GENERAL INFORMATION:
15 APPLICANT: VENTER, J. Craig et al.
17 TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
17 TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
17 TILE REPERENCE: CL01307

17 TILE REPERENCE: CL01307

17 TILE REPERENCE: CL01307

18 PRIOR APPLICATION NUMBER: 60/241,755

18 PRIOR PAPLICATION NUMBER: 60/231,498

18 PRIOR PELING DATE: 2000-10-20

18 PRIOR PELING DATE: 2000-10-30

18 PRIOR PILING DATE: 2000-09-08

18 NUMBER: FOR SEQ ID NOS: 207012

18 SEQ ID NO 14516

18 LENGTH: 203475
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Mismatches:
Indels:
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Matches:
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                            169 GlytysgluglugluglytystysArg 177
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NAME/KEY: misc_feature
NOCATION: (1)...(203475)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity:
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ORGANISM: Human
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LENGTH: 203475
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 14230

LENGTH: 13248
            US-09-949-016-12024/C
US-09-949-016-12024/C
Sequence 12024, Application US/09949016
Sequence 12024, Application US/09949016
Sequence 12024, Application US/09949016
Sequence 12024, Application US/09949016
GENERAL INFORMATION:
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR SEQ ID NOS: 207012
SOFTHARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 12024
LENGTH: 13248
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-949-016-14230/c
; Sequence 14230, Application US/09949016
; Patent No. 6812339
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Best Local Similarity:
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Best Local Similarity:
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US-09-949-016-12024
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Pred. No.:
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US-10-724-972A-6352 (1-335) x US-09-949-016-14519 (1-203475)
             PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEBSISE for Windows Version 4.0
SEQ ID NO 14519
LENGTH: 203475
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NAME/KEY: misc_feature

LOCATION: (1)...(203475)

OTHER INFORMATION: n = A,T,C or
US-09-949-016-14519
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Best Local Similarity:
                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                         Score:
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i Sequence 14518, Application US/09949016

i Patenn No. 6812339

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14518

LEWICH: 203475
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Sequence 14519, Application US/09949016

Sequence 14519, Application US/09949016

Fatent No. 6812319

Tatent No. 6812319

TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERRICE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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; LOCATION: (1)...(201475)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | NAME/KEY: misc_feature
| LOCATION: (1)...(201475)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14518
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Query Match:
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Best Local Similarity:
Query Match:
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FEATURE:
                                                                             Alignment Scores:
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Pred. No.:
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Conservative: Mismatches: Indels:

Gaps:

Length: Matches:

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ABOUT 17226/C

Sequence 17226, Application US/09949016

Patent No. 681239

Sequence 17226, Application US/09949016

Patent No. 681239

Sequence 17226, Application US/09949016

Patent No. 681239

SEGUENEAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17226

LENGTH: 203475
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Matches:
Conservative:
Mismatches:
Indels:
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i LOCATION: (1)...(203475)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-17226
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Best Local Similarity:
Query Match:
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US-09-513-999C-32507/c
                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 203475
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Alignment Scores:
Pred. No.:
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## Sequence 1728, Application US/09949016

## Sequence 1728, Application US/09949016

## Patent No. 681239

## GENERAL INFORMATION:
## APPLICANT: VENTER, J. Craig et al.
## TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## PRIOR REPERBENCE: CLOOD-0.04-14

## PRIOR PILING DATE: 2000-04-0.03

## PRIOR PILING DATE: 2000-10-03

## PRIOR PILING DATE: 2000-10-03

## PRIOR PILING DATE: 2000-09-08

## NUMBER OF SEQ ID NOS: 207012

## SEQ ID NO 17228

## LENGTH: 203475
                                                       Sequence 1727. Application US/09949016

Sequence 1727. Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL 307

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ THANKE: FRESE FRESE OF OF WINDOWS VEFSION 4.0

SEQ THANKE: PASSE OF OF WINDOWS VEFSION 4.0

SEQ ID NO 17227
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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OTHER INFORMATION: n = A, T, C or G
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LOCATION: (1)...(203475)
OTHER INFORMATION: n = A,T,C or
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2.69%
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Best Local Similarity:
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US-09-949-016-17228/c
                                                     -016-17227/c
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ORGANISM: Human
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## Patent No. 6783961
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| Patent No. 6783961
| FILE REFERENCE: 59.US2.REG
| CURRENT APPLICATION NUMBER: US/09/513,999C
| CURRENT FILING DATE: 2000-02-24
| PRIOR FILING DATE: 1999-02-26
| NUMBER OF SEQ ID NOS: 36681
| SOFTWARE: Patent.pm
| SEQ ID NO 2950
| LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-724-972A-6352 (1-335) x US-09-513-999C-2950 (1-352)
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Matches:
Conservative:
Mismatches:
Indels:
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US-005-513-999C-29145
'Sequence 29145, Application US/09513999C
'Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa=Asp or Glu
US-09-513-999C-2950
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LOCATION: 121
COCATION: 121
CTHER INFORMATION: 8=g OX
FEATURE:
NAME/KEY: misc_feature
LOCATION: 188
OTHER INFORMATION: m=a OX
FEATURE:
NAME/KEY: misc_feature
LOCATION: 189
OTHER INFORMATION: 8=g OX
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LOCATION: 111..350
FEATURE:
NAME/KEY: misc_feature
LOCATION: 119 OTHER INFORMATION: s=g o:
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: 260
OTHER INFORMATION: v=a
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Best Local Similarity:
Query Match:
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LOCATION: 27
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LOCATION: 50
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Patent No. 6476212

GENERAL INFORMATION:
APPLICANT: LALGUIN, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman. Bradley K.
APPLICANT: Sherman. Browner S.
APPLICANT: SHERMING POLYVEDIDES AND POLYPEPTIDES DERIVED FROM CORN EAR CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT APLICATION NUMBER: US/09/313,294A

CURRENT FILLING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL PROGRAM

SEQ ID NO 5824
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NAME/KEY: misc feature
CTHER INFORMATION: Incyte ID No. 6476212 700350739H1
US-09-313-294A-5824
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-513-999C-2950
; Sequence 2950, Application US/09513999C
SOFTWARE: Patent.pm
SEQ ID NO 32507
LENGTH: 181
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
LOCATION: 16
OTHER INFORMATION: r=a or g
FRATURE:
NAME/KEY: misc_feature
COTATION: 130
COTHER INFORMATION: s=g or c
FRATURE:
NAME/KEY: misc_feature
LOCATION: 130
LOCATION: 131
LOCATION: 131
OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-32507
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Percent Similarity: Best Local Similarity: Query Match: DB:

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Alignment Scores: Pred. No.:

TYPE: DNA ORGANISM: Zea mays

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

US-09-313-294A-5824

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Sequence 39108, Application US/09949016;
Sequence 39108, Application US/09949016;
Patent No. 681239
Sequence 39108, Application US/09949016;
Patent No. 681239
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: G0/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,408
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09
NUMBER OF SEQ ID MOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 39108
TUNNEND O 39108
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERBNCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
FRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2334
LENGTH: 564
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Myxococcus xanthus
PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(564)
US-09-902-540-2334
US-09-902-540-2334
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Best Local Similarity:
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ORGANISM: Human
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Pred. No.:
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Sequence 884, Application US/09328352
Sequence 884, Application US/09328352
Sequence 884, Application US/09328352
GENERAL INFORMATION:
APPLICAMT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENENCE: GT99-039-03-04
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 884
LENGTH: 390
 APPLICANT: Dunas Mille Edwards, J.B.
APPLICANT: Dunas Mille Edwards, J.B.
APPLICANT: Dunas Mille Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REPRENCE: 59.US2.REG
CURRENT FILING DATE: 59.US0.02-24
PRIOR PRILING DATE: 1999-02-24
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 29145
LENGTH: 378
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Matches:
Conservative:
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Matches:
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US-09-902-540-2334
; Sequence 2334, Application US/09902540
; Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA CORGANISM: Acinetobacter baumannii US-09-328-352-884
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LOCATION: 271

JOTHER INFORMATION: m=a or C

US-09-513-999C-29145
                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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US-09-328-352-884
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Pred. No.:
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RESULT 30

US-09-949-016-135038

Sequence 135038, Application US/09949016

Sequence 135038, Application US/09949016

Setent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER,
TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-00-01-0-20

PRIOR PRILING DATE: 2000-10-20

PRIOR PRILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

PRIOR FILING DATE: 2000-00-09

SEQUENCE FILING DATE: 2000-00-09

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SEQUENCE FILING DATE: 2000-09-09

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i Sequence 149234, Application US/09949016

i Sequence 149234, Application US/09949016

i Sequence 149234, Application US/09949016

i Patent No. 6812339

i TITLE No. INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i FILE REFERENCE: 2000-04-14

i PRIOR PLIING DATE: 2000-10-20

i PRIOR FILING DATE: 2000-10-20

i PRIOR FILING DATE: 2000-09-08

i NUMBER OF SEQ ID NOS: 207012

i SEQ ID NO 149234

i LENGTH. 601
                                        US-10-724-972A-6352 (1-335) x US-09-949-016-60204 (1-601)
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Human
US-09-949-016-135038
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US-09-949-016-149234
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                                                              US-09-949-016-60203/c

Sequence 60203, Application US/09949016

Sequence 60203, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: 60/241,755

PRIOR PLLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-09-08

NUMBER: 60/231,498

NUMBER: OF SEQ ID NOS: 207012

SEQ ID NO 60203

LENGTHARE: FASELSEQ for Windows Version 4.0

LENGTH: 61
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Sequence 60204, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION UNMER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOFTWARE: PRESENCE FRESENCE FRESENCE FRESENCE

LENGTH: 601
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Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
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; ORGANISM: Human
US-09-949-016-60203
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; ORGANISM: Human
US-09-949-016-60204
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Sequence 1850, Application US/09543681A
Sequence 1850, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: US/09102-001
TITLE OF INVENTION: US/09102-001
FILE REFERENCE: 2709.1002-001
CURRENT FAPLICATION WUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1850
LENGTH: 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14140

Sequence 14140

Sequence 14140

Sequence 14140

Sequence 14140

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Conservative:
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Matches:
Conservative:
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             Conservative:
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Indels:
   Matches:
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                                                                                                                                                     46 GCAGCCTGTGGCAACAATTCATCT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14140
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8.00
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; ORGANISM: Proteus mirabilis
US-09-543-681A-1850
                 100.00%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
      Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-270-767-14140
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Pred. No.:
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Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPLEMBLE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 909
LENGING SEQ ID NOS: 5674

LENGING SEQ ID NOS: 5674
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Patent No. 6703492

Patent No. 6703492

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT PELICATION NUMBER: US/09/710,279
CURRENT PELICATION NUMBER: 001-01-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PATENTING VET. 2.1

SEQ ID NO 1567
LENGTH: 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                           Conservative:
Mismatches:
Indels:
Gaps:
             Matches:
                                                                                                                                            24 AlaAlaCysGlyAsnAsnSerSer 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
, ORGANISM: Staphylococcus epidermidis
US-09-134-001C-909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 ecaeccierescaacaarrcarcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-09-710-279-1567
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Pred. No.:
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US-09-134-001C-909
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NAME/KEY: misc binding
| NAME/KEY: misc binding
| LOCATION: 502.7521
| O'THER INPORMATION: 12-515-394.mis2, potential complement
| NAME/KEY: primer bind
| LOCATION: 107..126
| O'THER INFORMATION: upstream amplification primer
| LOCATION: 537..557
| O'THER INFORMATION: downstream amplification primer, complement
| NAME/KEY: primer bind
| LOCATION: 489..517
| O'THER INFORMATION: 12-515-394 potential probe
| US-09-641-638-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc binding LOCATION: 502. 520
OTHER INFORMATION: 12-516-97.mis2, complement
NAME/KEY: Primer bind
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer bind
LOCATION: 891..91
OCATION: 691..91
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LOCATION: 501
OTHER INFORMATION: 12-516-97 : polymorphic base C or 'NAME/KET: misc binding
LOCATION: 481.500
OTHER INFORMATION: 12-516-97.misl, potential
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
OTHER INFORMATION: 12-515-394.mis1, potential
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ORGANISM: Homo Sapiens
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Best Local Similarity:
Query Match:
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                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PELLING DATE: 1090.01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2246
LENGTH: 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 37
US-09-641-638-192
i Sequence 192, Application US/09641638
j Patent No. 6432648
i GENERAL INFORMATION:
i APPLICANT: Bluemefeld, Marta
APPLICANT: Bluemefelt, Lydie
APPLICANT: Cohen, Annick
ITILE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
ITILE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
I TILE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
CURRENT FILING DATE: 2000-08-16
PRIOR PRICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 1999-05-11
PRIOR PLILING DATE: 1999-06-07
PRIOR PRILING DATE: 1999-06-07
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-12
PRIOR SEQID NOS: 1304
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
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NAME/KEY: allele
LOCATION: 12-515-394 : polymorphic base A or T
NAME/KEY: misc_binding
LOCATION: 481..500
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Matches:
Conservative:
Mismatches:
Indels:
 28 AsnAsnSerSerAsnSerSer 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678 GCCGTGGCTGCAAAAAGCGGACTG 701
                                                                                       US-09-489-039A-2246
; Sequence 2246, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2246
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8.00
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100.00%
2.39%
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ORGANISM: Homo Sapiens
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Best Local Similarity:
Query Match:
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US-10-724-972A-6352 (1-335) x US-10-170-097-192 (1-1001)
                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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LOCATION: 489..513
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ORGANISM: Homo Sapiens
                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                              Alignment Scores:
Pred. No.:
US-10-170-097-192
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                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 192, Application US/10170097

Sequence 192, Application US/10170097

Patent No. 6794143

GENERAL INPORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Cohen, Annick

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS

FILE REFERENCE: GRN-T114XC2D1

CURRENT FOLING DATE: 2002-06-10

PRIOR PAPLICATION NUMBER: US/10/170,097

CURRENT FILING DATE: 2000-08-16

PRIOR PAPLICATION NUMBER: US 60/133,200

PRIOR PLING DATE: 1999-05-07

PRIOR PLING DATE: 1999-05-07

PRIOR PLING DATE: 1999-03-23

PRIOR PLING DATE: 1999-03-23

PRIOR PLING DATE: 1999-03-13

PRIOR PLING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304

SEQ ID NO 192

LENGTH: 1001

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LOCATION: 537...557
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 502. 521
OTHER INFORMATION: 12-515-394.mis2, potential complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: 12-515-394 : polymorphic base A or
                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-724-972A-6352 (1-335) x US-09-641-638-193 (1-1001)
                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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LOCATION: 107..126
OTHER INFORMATION: upstream amplification primer
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NAME/KEY: misc_binding
LOCATION: 481..500
OTHER INFORMATION: 12-515-394.mis1, potential
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// LOCATION: 489..513
// OTHER INFORMATION: 12-516-97 potential probe
US-09-641-638-193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    717 AATTCTAGCTCTAACAGCTCTAAA 740
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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DB:
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LOCATION: 501
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US-10-170-097-192
                                                                                                                                                                             Alignment Scores:
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US-10-170-097-193

US-10-170-097-193

Sequence 193, Application US/10170097

Patent No. 6794143

Patent No. 6794143

Patent No. 6794143

APPLICANT: Blumenfeld, Marta

APPLICANT: Cohen, Marica

APPLICANT: Cohen, Annica

TITLE OF INVENTION: BLALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

TITLE OF INVENTION: GEN-71144XC2D1

TITLE OF INVENTION: GEN-7114XC2D1

TITLE OF INVENTION: GEN-7114XC2D1

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2000-08-16

PRIOR FILING DATE: 2000-08-16

PRIOR FILING DATE: 2000-02-11

PRIOR PALICATION NUMBER: US 69/502,330

PRIOR FILING DATE: 1999-05-07

PRIOR PLICATION NUMBER: US 60/133,200

PRIOR FILING DATE: 1999-05-07

PRIOR PLICATION NUMBER: US 60/133,200

PRIOR FILING DATE: 1999-05-07

PRIOR PLICATION NUMBER: US 60/133,200

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-12

PRIOR PLICATION NUMBER: US 60/119,917

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PRIOR PLICATION NUMBER: US 60/119,917

PRIOR PLICATION NUMBER: US 60/119,917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRATURE:
NAME/KEY: allele
LOCATION: 501
OCHER INFORMATION: 12-516-97 : polymorphic base C or T FEATURE:
NAME/KEY: misc_binding
LOCATION: 481..500
OTHER INFORMATION: 12-516-97.misl, potential
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NAMENTON: 405..424
OTHER INFORMATION: upstream amplification primer
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LOCATION: 502..520
OTHER INFORMATION: 12-516-97.mis2, complement
PEATURE:
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; OTHER INFORMATION: 12-516-97 potential probe
US-10-170-097-193
                                            923 AATTCTAGCTCTAACAGCTCTAAA 946
29 AsnSerSerSerAsnSerSerLys 36
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Length: Matches: Conservative: Mismatches: Indels: Gaps:	US-10-724-972A-6352 (1-335) x US-10-170-097-193 (1-1001)	rLyn 36	 AAA 740
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Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	-972A-6352 (1	29 AsnSerSer	717 AATTCTAGCTCTAACAGCTCTAAA 740
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Search completed: November 10, 2005, 03:07:59 Job time : 664 secs

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AX370197 Sequence
Continuation (46 o
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AE01733311 CP00000211 AE0060047 AX433651 AB082122 AP005009 BX595085111 BX55085112 AX933596 AX933596 AR354237 AR354237 AR354237 AR354237

Continuation (34 o AX583941 Sequence BD237137 Staphyloc AR28235 Sequence AF079518 Staphyloc AR354120 Sequence

AR282355 AF079518 AR354120

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AE016750 300698 bp DNA linear BCT 01-JAN-2003
Staphylococcus epidermidis ATCC 12228, section 7 of 9 of the
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Staphylococcus epidermidis ATCC 12228
Bacteria; Firmicutes; Bacillales; Staphylococcus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
Candy.Y., Ren.S., Li,H., Fu,G., Lu,L., Lu,G., Jia,J., Tu,Y., Din,Z., Chen,Z. and Wen,Y.
Direct Submission
Submitted (05-NOV-2002) Chinese National Human Genome Center at Shanghai, 250 Bl Bo Road, Shanghai 201203, China
Location/Qualifiers
I. 300698
| Corganism=Staphylococcus epidermidis ATCC 12228"
| Mol type="genomic DNA"
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U00096 45
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complement(114. .186)
/product="tRNA-Lys"
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/product="tRNA-Gln"
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN_E0 -ALIGN=40 -MODE=LOCAL
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT - SCRAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AP003136 Staphyloc
AP003364 Staphyloc
Continuation (24 o
                                                                                                             2005, 19:43:37 ; Search time 5171 Seconds (without alignments) 3139.141 Million cell updates/sec
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                                                                                                                                                                                 US-10-724-972A-6352
1690
1 GVESVRGLKILSVIGLLFVL.....EEMAKELVELSKKDSKKDNK 335
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                         - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                      4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                                                                                                                                                                      of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE016750
AP003136
AP003364
BX571856_23
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                       BLOSUM62
Xgapop 10.0 , Ygapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                           Run on:
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WVGIIFLPIIIMRTSWWFIFFIFLGGLSYTIGAMFVAQKNKRYFHMIWHIFIVLASFL
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Whole genome sequencing of meticillin-resistant Staphylococcus
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                                                       18764 TIGCCTGCAGTAGCTGCTAAATCAGGTTTGCTTGCTCATCCAAGCAACTCTTATGTTGGT
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Director-General, Biotechnology Center, Aoki,K., Oguchi,A.,
Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
Direct Submission
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Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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complement (2222 . .3247)
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hypothetical protein, similar to ribosomal-protein-alanine
N-acetyltransfer"
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On Apr 16, 2004 this sequence version replaced gi:14247707.
This work was done in collaboration with Toshiko Ohta, Mutsumi Kanamori, Hideo Hayashi (University of Tsukuba), Hideki Hirakawa, Satoru Kuhara (Kyushu University), Ikuo Uchiyama (Okazaki National Research Institutes), Susumu Goto, Minoru Kanehisa (Kyoto University), Naotake Ogasawara (Nara Institute of Science and Technology) and supported by the Research for the Future Program of the Japan Society for the Promotion of Science.
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DNA_RESEARCH 11, 51-56 (2004)
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Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.
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Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.
Submitted (28-FEB-2011) Masahira Hattori, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@genome.ls.kitasato-u.ac.jp, Tel:81-42-778-8194,
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aureus Mu50 DNA, complete genome
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Best Local Similarity:
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complement (2027. .3457)

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Staphylococcus aureus
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COO7 01.00.00

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Best Local Similarity:
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SerSerAsnGluProSerLeuLy8GluLeuGluLy8AspPro---ValTrpLy8Ly8Leu 290
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730 AATGAAGAACTTGCCAATATCAATCCAAAAGTTATGATTTTAGCCACTGACGGAAAAACG 789
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Sequence 301 from Patent WO02059148.
AX583924
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GlugiyLysiysArgieuGluHisAspLysLysIleGluGluTyrLysLysGluile 192
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790 GACAAAAATAGAACGAAATTCATTGATCCTGCAGTTTGGAAATCATTA 8 291 AsnalaValLysAsnGlnargValAsplieLeuAspArgAspLeuTrpAlaArgSerArg 3	Staphylococ Staphylococ Bacteria; B Masignani, V Staphylococ Patent: Wo Chiron Spa Lc	Alignment Scores: Pred. No.: 1.07e-45 Matches: Score: Percent Similarity: 66.67\$ Conservative: 63 Best Local Similarity: 42.87\$ Mismatches: 95 Query Match: 6 Gaps: US-10-724-972A-6352 (1-335) × AX621226 (1-975) Qy 13 ValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCygGlyAsnAsnSerSerSer 32	AsnSerSerLyaGluSerSerLysAspGlyValGlulleLysHisGluGluGlyThrThr	3 1 3 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

gene

CDS

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This work was done in collaboration with Toshiko Ohta, Mutsumi Kanamori, Hideo Hayashi (University) of Tsukuba), Hideki Hirakawa, Satoru Kuhara (Kyushu University), Ikuo Uchiyama (Okazaki National Research Institutes), Susumu Goto, Minoru Kanehisa (Kyoto University), Naotake Ogasawara (Nara Institute of Science and Technology) and supported by the Research for the Future Program of the Japan Society for the Promotion of Science.
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Whole genome sequencing of meticillin-resistant Staphylococcus
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Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.
Direct Submission
Submitted (28-FEB-2001) Masshira Hattori, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@genome-18.kitasato-u.ac.jp, Tel:81-42-778-8194, Par.81-42-778-8193)
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Yamashita,A., Oshima,K., Kuroda,M., Hattori,M., Hiramatsu,K.,
Kubara,S. and Hayashi,H.
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AP0033361 BA0000017
AP003361.3 GI:46395333
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Staphylococcus aureus subsp. aureus Mu50
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POLYNUCLEOTIDES AND AMINOACID SEQUENCES FROM STAPHYLOCOCCUS AUREUS
PATENT: WO 9731114-A 10 28-AUG-1997;
SMITHKLINE BEECHAM PLC (GB)
Location/Qualifiers
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                                GlyLeuIleSerSerGluGluWetAlaLysGluLeuValGluLeuSerLysLys 328
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Homologous recombination into bacterium for the generation
polynucleotide libraries
Patent: WO 03095658-A 20 20-NOV-2003;
Novozymes A/S (DK)
Location,Qualifiers
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                                                                                                                         TGCTGAGCATGATAAATTCAATAAGTATAAAGATGAAATTAAATTTGATAGAAATCA
                              198 niysvalleuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTy
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                                                                                                                                                      nValAsnProGluArgMetPheileMetThrAsnLysAlaSerSerAsn 274
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Mismatches:
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Submitted (09-JUL-1996) Junichi Sekiguchi, Textile Science and Technology, Shinshu University, Department of Applied Biology; 3-15-1 Tokida, Ueda-shi, Nagano 386, Japan (E-mail: jeskigagiptc.shinshu-u.ac.jp, Tel:0268-21-5344,
                                                                                                                                           ArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGlu 324
                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Sekiguchi, J.
Direct Submission
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LCKL QSFGI PYLSGI SPFKRDEVKDI FVRAPWWTMTRR PGTYSRGNGGKGAKREDPKD
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SOURCE
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                                      25123 ATTGCCATCATGAGTGTTTA---TTGCTCGCCTGCTCATTGTATCCGGCTGTTCATCA 25179
                                                                                                                                                                        25180 AGCCAGAATAACAACGGAAGCGCAAAAGCGACTCTAAGGATTCCAGAGTGATCCATGAC 25239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu 147
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           LeuLysileLeuSerValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGly
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Bacillus subtilis subsp. subtilis str. 168
Bacillus subtilis subsp. subtilis str. 168
Bacteria, Firmicutes, Bacillales, Bacillaceae; Bacillus.

I (bases 1 to 19740)

Runst, F., Ogasawara, N., Moszer, I., Albertini, A., M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotchin, A., Borchert, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Commerton, I.F., Cummings, N. J., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N. J. Daniel, R.A., Denizoto, F., Pujita, M., Pujita, Y., Fuma, S., Galizzi, A., Galleron, N. Ghin, S.Y., Glaser, P., Goffeeu, A., Golightly, B.J., Galleron, N., Ghin, S.Y., Glaser, P., Mosono, S., Hullo, M.F., Hibert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kashara, Y., Kaerre-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Mello, S., Mauel, C., Medigue, C., Medina, N., Mellado, R.P., Mizuno, M., Mestil, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwera, A., Odiega, B., Rescott, A.M., Prescean, E., Pujic, P., Nivoles, E., Schleich, S., Schroeter, R., Scoffene, F., Sekiguchi, J., Sarolan, E., Schleich, S., Serror, P., Shin, B., Soldo, B., Sorowkin, A., Tacconi, E., Tanaka, T., Terpstra, P., Tosacott, A., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Viati, A., Viati, A., Viati, A., Viati, A., Viati, A., Viati, A., Volkika, M., Viati, K., Yoshikawa, H. F., Zumstein, E., Yoshikawa, H. F., Zumstein, E., Yoshikawa, H. F., Zumstein, E., Yoshikawa, H. P., Zumstein, R., Yoshikawa, H. P., Zumstein, E., Yoshikawa, H. F., Zumstein, R., Yoshikawa, H. and
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This entry contains data from release R16.1 of the Subtilist
database. Further data on gene annotation and detailed information
about changes from previous releases can be found at
http://genolist.pasteur.fr/SubtiList/.
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Direct Submission
Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur,
Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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Nature 390 (6657), 249-256 (1997)
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Bacillus subtilis complete genome (section 5 of 21): from 813670 to 1011078.

Z99108 AL009126 Z99108.2 GI:32468715

ACCESSION VERSION KEYWORDS

BSUB0005/c LOCUS DEFINITION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="yfmK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LeulysileLeuServallleGlyLeuLeuPheValLeuileAlaThrAlaAlaCysGly 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 GluGluGlyThrThrbysValProLysHisProLysArgValValValLeuGluTyrSer
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149
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103
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Mismatches:
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679.50
62.78%
47.00%
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DB:
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924. . 1916
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- 21.0.
                                                                        3 (bases 10610 to 12556)
van Sinderen,D., ten Berge,A., Hayema,B.J., Hamoen,L. and Venema,G.
Molecular cloning and sequence of comK, a gene required for genetic
competence in Bacillus subtilis
Mol. Microbiol. 11 (4), 695-703 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Similarity to several hypothetical proteins, from
Haemophilus influenzae (Swiss Prot P44036), Saccharomyces
cerevisiae (Swiss Prot P39979), and others."
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/gene="yhfQ"
/note="Similarity to citrate-dependent iron transport
protein fece from E.coli (PIR S56515) and Synechocystis
sp. (EMBL: D90899)."
                                                                                                                                                                                                              4 (bases 1 to 12556)
Noback, M.A., Terpstra, P., Holsappel, S., Venema, G. and Bron, S.
Direct Submission
Submitted (26-UM-1997) Noback M. A., University of Groningen,
Dept. of Genetics, Kerklaan 30, Haren, 9751 NN The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:1423"
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                  J. Bacteriol. 171 (5), 2657-2665 (1989)
89213955
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907. .919
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2043. .2056
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                                                                  12201 TTCTTGGATGCCGTTCACAATCTCGGCATTACGCCGGTGGGCATCGCAGATGACAACAAA 12142
                                                                                                                                             11784 GATTCCTTCCAGCTTCATACATCATCCTATGACGGAGAAATCTTTAAAATGCTAGGC 11725
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11583 AAAAATCTCAAAGGGTGAAAATGGACAAGTCTATGATGCGGACCGTGACACTTGGACA 11524
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Park,S.S., Wong,S.L., Wang,L.F. and Doi,R.H.
Bacillus subtilis subtilisin gene (aprE) is expressed from a sigma A (sigma 43) promoter in vitro and in vivo
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region 78-80 degrees: aprE to
                                       LysAsnargilelleLysProLeuArgAspLysileGlyLysTyrThrSerValGlyThr
                                                                                                                    ArgLysGlnProAsnLeuGluGluileSerLysLeuLysProAspLeuIleIleAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                           188 TyriysiysiyileThrMetAspiysAsnGlniysValLeuProAlaValAlaAlaLys
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1 (bases 1 to 104)
Stahl.M.L. and Ferrari, E.
Replacement of the Bacillus subtilis subtilisin structural gene with an In vitro-derived deletion mutation
J. Bacteriol. 158 (2), 411-418 (1984)
                                                                                                                                                                                                    AsnAsnArgHisLysGly1leTyrLysAspLeuAsnLys1leAlaProThr1leGluLeu
                                                                                                                                                                                                                                                                               148 LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrileSerLysAla
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ComK Gene; yhfO gene; yhfP gene; yhfQ gene; yhfR gene; yhfS y
yhfT gene; yhfU gene; yhfV gene; yhfW gene; yhxC gene; yhxD g
Bacillus subtilis
Bacillus subtilis
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| 11724 TTTACACACGCTGTGAAGTCAGAT------
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Bacillus subtilis chromosomal DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                           /gene="yhf8"
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complement(6325. .6885)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
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xref="UniProt/TrEMBL:007619"
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complement(6329. .6336)
                                                                                                                                                                                                                                                                                                          complement (4893. .4903)
/gene="yhfS"
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B.subtilis (EMBL: Z75208), bile acid-CoA ligase from
Eubacterium sp. (Swiss Prot P19409), long-chain-fatty
aciduCoA ligase from E.coli (LcfA; Swiss Prot P29212)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            force. Similarity to a hypothetical protein 0215b from E.coli (Swiss Prot P36942), and to several phosphoglycerate mutase (pgm) proteins, from Treponema pallidum (EMBL: U55214) and Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product = "hypothetical protein"
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Bacillus subtilis subsp. subtilis str. 168
Bacillus subtilis subsp. subtilis str. 168
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

1 (bases 1 to 198743), Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, K., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Ettian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fabret, C., Ferrari, E., Galleron, N., Ghin, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Hallo, M. F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Koatter, P., Klaer-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Liu, H., Masuda, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Media, N., Nellado, R.P., Masuda, S., Mauel, C., Medigue, C., Media, N., Park, S.H., Parro, V., Pohl, T.M., Ogawa, K., Ogiwara, A., Odega, B., Park, S.H., Parro, V., Pohl, T.M., Porretelle, D., Porwollik, S., Prescott, A.M., Parro, V., Pohl, T.M., Purnelle, B., Rappoport, G., Reo, M., Sadaie, Y., Sekiguchi, J., Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J.,
                                                                                                  2610 GTCGGCAAGGAAAGGAAAATGGAGAAAAAGCTGACGGCGCATGAAGAAAAGCTTAGCGAG 2669
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2670 ACAAAGCAGAAAATCAGCGCGAAC---AGCCAGTCCGTGCTTTTGATCGGAAATACAAAT 2726
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2787 TACCGATATGCAATCAGT-----ACGTCAGGCAATAGCGATTCAAGCAATGGGGGC 2837
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2898 ATCCTGATGACAGGAAAAACAGATGACCTCGACGCCGACGGTAAACGCCCGATCGAAAAG 2957
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                                                                      LeuGlytysegluglugluglyLystysArgLeuGluGluHisAspLysLysIleGluGlu
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On Jul 7, 2003 this sequence version replaced gi:2633260.
This entry contains data from release R16.1 of the SubtiList database. Further data on gene annotation and detailed information about changes from previous releases can be found at http://genolist.pasteur.fr/SubtiList/.
Location/Qualifiers
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Yasuhida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur, Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1
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Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 198741)
Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
Direct Submission
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'function="cell wall lytic activity"
'note="alternate gene name: cwlE, yhdD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1657. .2097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="BSU09370"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="yhdE"
                                                                                                                                                                                                                                                                                                                                                              Danchin, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 AsnAsnArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaProThrileGluLeu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 ArglysGlnBroAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAsp 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 LeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 TyriysLysGluileThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LysileLeuSerValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 AsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 GluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96116 TTAGGGAAGACAAATGTGCCTGAGCATCCGAAGCGGGTTGTTCTTGTTCTTGAGCTAGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 ValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96176 ATTGATACACTGCTTGATCTCGGCATTACGCCTGTCGGGGTTGCCGATGACAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 AsnArgileije---LysProLeuArgAspLysileGlyLysTyrThrSerValGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198743
136
70
113
16
                                                                                                                                                           /function="cell wall lytic activity"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-724-972A-6352 (1-335) x BSUB0006 (1-198743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (8292. .9218)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.53e-34
613.00
61.49%
40.60%
36.27%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
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                                                  CDS
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|11532 AAATATTTTGCTATTTTTATTGATGATGATGATGATGACGGCCTGCTCTGGA---
                                                                                                                                                                 29 AsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGlu
                                                                                                                                                                                                 89 AsnArgileileLysProLeuArgAspLysIleGlyLysTyrThrSerValGlyThrArg
                                                                                                                                                                                                                                                                                                                                       AsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLys
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|12063 AAACAGAAATTCGGC---AGCCGGAAACAGAGCATTCTTCTGCTCGGGAACACAAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPhe
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Matches:
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                                          TACCGATATGCAATCAGT-----ACGTCAGGCAATAGCGATTCAAGCAATGGCGC 96703
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                                PhelysGluhlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGly--- 246
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                                                                                                            SerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGly
                                                                -----ProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMet
                                                                               GACTCTGTGAATATGAAATGACACTGGAGCAGCTGCTGAAAACAGATCGGATGTGATC
                                                                                                PhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu---LeuGluLys
                                                                                                                                  AspProvalTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg
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AE006047 AE004439
AE006047.1 GI:12720328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 ArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGlu---LeuSer 326
                                                                                                                                                                           LysginproAsnLeuGluGluileSerLysLeuLysProAspLeuIleileAlaAspAsn 128
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                                                                                                                                                      <u>AAGTTTÄTTAACGAGAAAGGTCÄĞĞĞĞAAAATCAAAĞĞĞTÄTÄCTTCÄĞTCĞĞTTTCĞĞĞ</u>
                                                                                                                                                                                        10789 CTTGGAGAAACGAAAGTGCGGAATAAACCGAAAAAAGTTGTGGGTTCTTGAATTGGGATTT
                                                                                                     10849 ATTGATGCGCTCCTTGATGCGGGTATTAAGCCTGTCGGAATTGCGGACGACGACGACCAACCT
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                                                                                        69 ValAspAlaLeuValAlaLeuAspValLysProValGlylleAlaAspAspAsnLysLys
                                                                                                                                  AsnArgilelleLysProLeuArgAspLysileGlyLysTyrThrServalGlyThrArg
     AsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGlu
                                              49 GlugiyrhrthygvalProLysHisProLysArgvalvalvalLeuGluTyrSerPhe
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3834. .5189

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RKYTLILANNARTAGBLRGSGDATAAKVFSDAFSQEPYSFLRSLKAYESSFANSDN
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Pm70"
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Pasteurella multocida subsp. multocida str. Pm70
Pasteurella multocida subsp. multocida str. Pm70
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellacea; Pasteurella.
1 (bases I to 1392)
May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S. and Kapur, V.
Complete genomic sequence of Pasteurella multocida, Pm70
Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (24-OCT-2000) Department of Veterinary Pathobiology,
University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="synonym: PM0118"
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2 (bases 1 to 13792)
Zhang, Q. and Kapur, V.
                                                       ORGANISM
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AUTHORS
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TITLE
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------CAACCTAATGCTTCGGTTTAGAACAAGTGGCGGCAGAAAG 12922
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13245 CCGACAGTCGTCTTTAATTCCCGCCATGAGAACTATCAAGAAAACCTTGAAACCGCACAA 13186
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13365 GAATCAGTGGGGACGCGTTCTCAACCGAGTTTAGAAGCGATTTCTGCACTTAAACCAGAT 13306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 LeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIle 300
                                                                                                                                                      163 ThrileSerLysAlaLeuGlyLysGluGluGluGluGlyLysLysArgLeuGluGluHisAsp 182
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                                                                                                                                                                                                                                                                                 203 AlavalAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe
                                LeullelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAla
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Methods for monitoring multiple gene expressivethods for monitoring multiple gene expressivencent: WO 0229113-A 2066 11-APR-2002;
Novozymes Biotech, Inc. (US); Novozymes A/S Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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Sequence 2066 from Patent WO0229113.
AX433651
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Tanabe, T., Funahashi, T., Nakao, H., Miyoshi, S., Shinoda, S. and Yamamoto, S. Identification and characterization of genes required for biosynthesis and transport of the siderophore vibrioferrin in Vibrio parahaemolyticus J. Bacteriol. 185 (23), 6938-6949 (2003) 22982453 14617658 2 (bases I to 4044) Yamamoto, S., Tanabe, T. and Funahashi, T. Direct Submission Submitted (22-MAR-2002) Shigeo Yamamoto, Okayama University, Faculty of Pharmaceutical Sciences; 1-1-1 Tsushima-naka, Okayama, (E-mail:syamamoto@phesaant.pharm.okayama-u.ac.io.		/producte="ferric vibrioferrin-binding periplasmic protein prubus paula" /protein id="BAC16540.1" /db_xref="G1:23307110" /db_xref="G1:23307110" /fb_xref="G1:23307110" /fb_xref="G1:23307110" /fb_xref="G1:23307110" /fb_xref="G1:23307110" /franslation="MKNKKOFTIKHESTVLIMLLSSVFMSFSALSQARSVQDEGGTFE LBAIPQRIVEDETSFVDALAAVDSPVQSPAGADDNDARTRIPIPATARIEPMOSYGMSQP SLEAIAVLKPDLIIADAEBRHAIYODLGRIAPTLLLKSRGETYGENLSSAGKICVAIG KQAQMTQRIELHRGTMAEFKQHFATQETIGFGSVSDRUHNBERKNPLFKLLTAAKKRQL 1076. 2113 /gene="pvuc" /cdcn start=1 /transl_table=11 /product="ferric vibrioferrin transport system permease /protein pvuc" //cotsin id="management" //cotsin id="managem		/codon_start=1 /trans_ tabhe=11 /product="ferric vibrioferrin transport system permease product="ferric vibrioferrin transport system permease protein pvuD" /protein id="BAC16542.1" /db_xref="G1:23307112" /db_xref="G1:23307112" /translation="MMNGIKLMALIGILLIASSLTLFVGAANLSAQQVFALLFSFSDS DFVIHQYRLPRMILAIGVGAGLGLSGVLVQGVIRNPLASPDLMGISAGAGLAATACLV LYPRAPAMLPNYAMAGGLLAAGFIAVLAXYWSKRTPARLALIGVANSAFVASGIDFLL IVHPIBINTANWALTGSLWGRNWQQVPFIAWALLILLILLPLAFWLANRLDVMGLGEESAT TLGTKRKQ1Q1LALIAANLLASISVSYNGTISFVGLLAPHLARLLFGHNHKLLIPASA TLGALLVICADGLARGLQPFIELPAGVLTSVIGAPYFIFLLYRYRGW" 30843848
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Query Match: 30.21\$ Indels: 3 DB: 6 Gaps: 3 US-10-724-972A-6352 (1-335) x AX433651 (1-801) Qy 60 ArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysBro 79 1::			QY 279 LyBGluLeuGluLyBAspProValTrpLyBLyBLeuAsnAlaValLyBAsnGlnArgVal 298 Db 657 AGACCGATCGAAAAGATCCTCTTTGGAAAAGCTCAGCGCAGTCAAAAACGGCAAGGTT 716 Cy 299 AsplleLeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMet 318 Db 717 TATGAAGCCGACAGATTCGCCTCGTCGCTCCGACGCAGAGTTGACGAGATGAGCTG 776 Qy 319 AlaLysGluLeu 322 Db 777 ATGGATGAAATT TAT ATGGATGAAATT 788	RESULT 25 AB082122 4044 bp DNA linear BCT 21-NOV-2003 LOCUS LOCUS AB082122 4044 bp DNA linear BCT 21-NOV-2003 DEFINITION Vibrio parahaemolyticus ferric vibrioferrin transport system gene cluster (pvuB, pvuC, pvuB), complete cds. AB082122

830

1055

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Hattori,M., Yamashita,A., Oshima,K. and Shiba,T.

Stantori,M., Yamashita,A., Oshima,K. and Shiba,T.

Direct Submission

Submitted (09-APR-2002) Masahira Hattori, Kitasato Institute for Life Stantagawa 220-8555, Japan

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Pax:81-42-778-8193)

This work was done in collaboration with Kozo Makino, Ken Kurokawa,

Katsushi Yokoyama, Takayuki Uda, Kenichi Tagomori, Masatomo Najima,

Katsushi Yokoyama, Takayuki Uda, Kenichi Tagomori, Masatomo Najima,

Katsushi Honda, Hideo Shinagawa, Tetsuya Iida (Osaka University),

Tokatio Iijima (Kobe Institute of Health), and supported by the

Promotion of Science. This clone was isolated from a patient

presenting with acute gastroenteritis.
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Tagomori, K., Iijima, Y., Najima, M., Nakano, M., Yamashita, A.,
Kubota, Y., Kimura, S., Yasunaga, T., Honda, T., Shinagawa, H.,
Hattori, M. and Iida, T.
Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V cholerae
Lancet 361 (9359), 743-749 (2003)
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Vibrio parahaemolyticus DNA,
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Bacteria, Proteobacteria;
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Conservative:
Mismatches:
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               Patent: WO 03087377-A 1 23-OCT-2003;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR); INSTITUT NATIONAL DE LA RECHERCHE
AGRONOMIQUE (INRA) (FR)
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INSECTICIDE PROTEINS FROM PHOTORABDUS LUMINESCENS
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Procerhabdus luminescens subsp. laumondii TTO1 complete genome;
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Submitted (23-APR-2003) L. Frangeul, Institut Pasteur, Genopole, 25
rue du Docteur Roux, 75:24 Paris Cedex 15, FRANCE. E-mail:
lfrangeu@pasteur.fr, fkunst@pasteur.fr
Location/Qualifiers
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AAYGARAQGVGVASAAGAVTGAVGSWINNADRGIGGAIGAGSAVGTIDTMLGTSSTLT
HEVAAAAGGAAGGMITGTQGSTRAGIHAGIGTYYGSWIGFGLDVASNPAGHLANYAVG
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Photorhabdus luminescens subsp. laumondii TTO1
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duchaud, E., Frangeul, L., Rusniok, C. and Kunst, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Biotechnol. 11 (1) (2003) In press
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BX571873.1 GI:36787441
Complete genome.
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7709 GTAAAATC 7701
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331881 GTAAAATC 331889
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                                                                                                                                                             /notes"unnamed protein product; Similar to pyocin S3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product; Some similarities with pyocin S3 immunity protein and similar to Photorhabdus
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102
60
107
14
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Pred. No.:
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gene

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Length: Matches: Conservative: Mismatches: Indels:

5.99e-24 476.00 57.24% 36.04% 28.17%

Percent Similarity: Best Local Similarity:

gene

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Query Match

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331710 TGGCTTATCGTGGCCCACTATCGT-----CAGGAAAGCATCGTGAAACGCTGGCAG 331760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331821 AGCAACACCTGGGCTCGTATGCGCGGGATATTTGCCGCTGAACGCATTGGCAGCGATGCG 331880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331557 GGCACCTCGCGCGAACAGCAATTTAACCTGCACCACGATACCTATACCGGCAGCGTC 331616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331656 -----CATGCGGCAATGTTTCTCTCAACCTGGAACAGTTACTGGCACTCAATCCTGAC 331709
                                                                                                                                                                                                                                                                                                                                                                                                                     331443 ATCATCGGCAAAGTCATGGGGAAAGAGAGTGAGAAAGGGCTGGCAGAAGGCACGCT 331502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 ArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeu 322
                                                                                                                                                                                                                                                                                                                                                                                          142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 ProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLys 162
                                                                                                 82
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|CTGTCCTGCTAAAATCCCGCAACGAAACCTACGAAGAGAACCTGCAATCTGCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 TyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 ArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGlu
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                                                                                                                                                                                                                         331203 GCCGATGATAACGATCCGCAGCGATCTCTCACCGATGTTCGCCAGCGTATAAGCCCTGG
                                                                                                                                                                                                                                                                                                                        331263 CAATCAACCGGCACTCGCGCCCAACCAAGCCTTGAAGCCATCAGCGCGCTGAAACCTGAT
                                                                                                                             103 ThrservalGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAsp
                                                                                                                                                                                                                                                                                                                                                                                       LeulleIleAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLysIleAla
                                   ValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyile
                                                                                                                                                                                              AlaAspAspAspLysLysAsnArgllelleLysProLeuArgAspLyslleGlyLysTyr
43 ValGlulleLysHisGluGluGluThrThrLysValProLysHisProLysArgValVal
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TITLE JOURNAL FEATURES

REFERENCE AUTHORS

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ECOFECECDE 4842 bp DNA linear BCT 26-APR-1993 K-12 fecA gene, 3'end; fecB,C,D,and E genes, complete cds's.
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Escherichia coli

Escherichia coli

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

I (bases 1 to 4842)

Staudenmaier, H., Van Hove, B., Yaraghi, Z. and Braun, V.

Nucleotide sequences of the feeBCDE genes and locations of the

proteins suggest a periplasmic-binding-protein-dependent transport

mechanism for iron(III) dicitrate in Escherichia coli

Bacteriol. 171 (5), 2626-2633 (1989)
                                                                                                                                                                                                                                                  310 ArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAsp 329
                                                                                                                                                                                                                                                                                                                                                                                                                       302 CGTGGCTTAATTTCTTCTGAAGAAATGGCTAAAGAACTTGTTGAATTATCAAAAAAGAA 361
                                                                                                                  230 GlualaieuSeraspaspvalThriysGlyieuSeriysTyrieuiysGlyProTyrieu
                                                                                                                                                                                                                                  GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsn
                                                                                                                                                                                                                                                                                         270 LysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source text: Escherichia coli (strain K-12)
Location/Qualifiers
             91
16
0
0
        Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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86.89%
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28.11%
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                   Percent Similarity:
Best Local Similarity:
Query Match:
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|182 CATGCTAAAAAAGATTCTGCTGAATTCAAGAAGTTACAAGAAGATGCAACATGGAAAAAG 241
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Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and Scan, C.A.

Staphylococcus aureus polynucleotides and sequences

Patent: US 6737248-A 355 18-MAY-2004;

Location/Qualifiers
             1 (bases 1 to 668)

Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and Rosen,C.A.

Staphylococcus aureus polynucleotides and sequences

Patent: US 6593114-A 355 15-JUL-2003;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                          210 LeuLeuAlaHisProSerAsnSerTyrValQlyGlnPheLeuSerGlnLeuGlyPheLys
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REFERENCE AUTHORS

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Enterobacteriaceae; Shigella.

I (bases 1 to 66714)

Luck, S.N., Turner, S.A., Rajakumar, K., Sakellaris, H. and Adler, B. Perric dicitrate transport system (Pec) of Shigella flexneri 2a YSH6000 is encoded on a novel pathogenicity island carrying multiple antibiotic resistance genes

Infect. Immun. 69 (10), 6012-6021 (2001)
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                                                                                                                                             145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile
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                    105 valglyrhrargLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle
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CP4-57 of Escherichia coli K-12"
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Luck,S.N., Turner,S.A. and Rajakumar,K.
Direct Submission
Submitted (06-DEC-2000) Microbiology, Monash University, VIC 3800,
                                                                                                                                                                                                                              3 (Dases 1 to 66714)
Luck S.N., Turner, S.A. and Rajakumar, K.
Direct Submission
Submitted (17-MAY-2002) Microbiology, Monash University, VIC 3800,
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8, 2002 this sequence version replaced gi:15808696.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence updated by submitter d'hosses 1 to 66714)
Luck, S.N., Turner, S.A. and Rajakumar, K.
Direct Submission
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38594 GATCCGCTCTGGCGATGTTAACCGCCGCAGAAGCAGCAGAGCAGCTTCGCTTCGGTCGACAGT 38535
                                                                                                                                      38795 TCACGCGAACAGCAATTCAACCTGCATACTCAGGAGCCTGGACCGGCAGCGTGCTGGCC 38736
38909 GGCGAAATGGTGGTAAAAGCGAGAGATGCAGGCACGTCTGGAACAACATAAAGAGAGG 38850
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                                185 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 204
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                        GlnieuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu
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                                                                  38849 Arggegerargagecagecage ----- cricchaagga cacacagageratragecaca
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Mismatches:
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/db_xref="taxon:562"
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Sequence 14 from Patent WO0170776.
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="streptomycin adenyltransferase AadA1"
/product="streptomycin adenyltransferase AadA1"
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complement (17075. .17905)
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SPPUDVILIIMTVVVVAASALQAAGGWUYLRYGRFRRRPKYKYNIITAFFTIRWSWTIM
MGGFFLYSTLDVIAAVESGIRPSRTLAGSVVASQVALSGSPISAAMAAMITIMEN
NGVSFIQWSVCLPTSRAAMVAAFTARRQGCELQDDSYLERLQKGLVQKYENNSSI
KPGATLSVGLFLLATVAIVILAAFPQLRSPGFDIGKPWETRBILIITGCAACLWVLC
YTATDAILITETSFRAGWSSAVILGITUTGTTFIDAHLTEIKDIAGDILQAYPMLLAL
VLRGTGALLYSQGATTPLIIPLAVALDVPTWALLASYVAVTGVFVLPTYPTSLAAMEF
DTTGTTRVGKYVLNHPPMLPQLGGIAAGVALGFVIAPMII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                /note="confers streptomycin and spectinomycin resistance; similar to AadAl from Tn21 on plasmid R100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                           /producE="putative anaerobic decarboxylate transporter"
/protein_id="AAL08434.1"
/db_xref="GI:15808705"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 ValGlyThrArgLysGlnProAsnLeuGluGlulleSerLysLeuLysProAspLeulle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp
            note="Orf9; similar to DcuA in Escherichia coli K-12"
                                                                                                                                                                                                                                                           complement(<14553. .>15322)
/note="remnant of IS600-like element; central region
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Matches:
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                                                                                                                                                                                                                                                                                                           complement (15323. .16090)
/note="IS1 element"
complement (16171. .16962)
/qene="aaaaa"
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/gene="aadA1"
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7675 GAACTCTCGTTCGCCGATGCGCTGGCCGTGGACGTCATCCCGATCGGTATTGCCGAC 7616
                                                                                            7201 TCTCTGGGGCTG------AAGGTTCCCGCTGCGATG 7172
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                                                                                                                    145 IleGluieulysserPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile 164
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                           105 ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeulle
                                                            AspAsnLysLysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSer
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4600001 4639675
47) of U00096 from base 4500001 (U00096 Escherichia coli K-12 MG165
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|12142 GATAACGATGCAAAACGCATCCTGCCCGAAGTGCGTGCGCACCTGAAACCGTGGCAGTCC 12083
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Matches:
Conservative:
Mismatches:
Indels:
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/map="92.8 to 100 minutes"
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                                                                                                             11789 TCACGCGAACAGCAATTCAACCTGCATACTCAGGAGCTGGAACCGGCAGCGTGCTGGCC 11729
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Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.
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This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattener, director) at the University of Wisconsin-Medison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps with other sequence determined are annotated. The start of this entry overlaps the end of the entry ECUWW89 (100006) by 1885 bp.
                                                                                                                                                                                                                                                                                                                               264 MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys 283
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                                                                                    205 AlaalaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
    IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 204
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1 (bases 1 to 338534)

Burland, V., Plunkett, G. III, Sofia, H.J., Daniels, D.L. and
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Direct Submission
Submitted (22-AUG-1994) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                          ...----AACGTTCCCGCTGCGATG
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Nucleic Acids Res. 23 (12), 2105-2119 (1995)
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/db_xref="taxon:562"
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U14003.1 GI:1263172
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AUTHORS
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/nore="Tins sequence comparises the following lambda clones: DD928(EC27-278), DD930(EC30-188), CD928(EC27-1320), DD932 (EC30-188), CD933 (EC27-1070), DD933 (EC27-1070), DD943 (EC27-169), DD945 (EC37-169), DD945 (EC37-169), DD945 (EC37-169), DD952 (EC37-169), DD952 (EC37-169), DD952 (EC37-169), DD956 (EC37-167), DD956 (EC304-34), DD970 (EC30-202), DD974 (EC30-61), DD976 (EC304-4pp), DD977 (EC304-7), DD997 (EC304-7), DD997 (EC304-7), DD997 (EC304-7), DD997 (EC304-3), DD997 (EC304-3), DD997 (EC304-3), DD997 (EC304-3), DD997 (EC304-3), DD997 (EC304-3), DD997 (EC304-3), DD997 (EC304-15), DD997 (EC30-13); M13mp19 or Janus vectors were used for subcloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /procein id="AAA96987.1"
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KKVRDISFSVCRGEILGFAGLVGSGRTELMNCLFGYDKRAGGEIRLMGKDISFRSPLD
KKVRDISFSVCRGEILGFAGLVGSGRTELMNCLFGYDKRAGGEIRLMGKDISFRSPLD
RELLALKCHSVNQNTTELSGGNQGVVLISKNLCCCPRVIIPDEPTRGIDVGAAREIV
VMRQLADDGKVILMVSSELPEIITVCDRIAVFCEGRLTQILTNRDDMSEEEIMAMALP
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MLDAKVIIMDEPTSSLTNKEVDYLFLIMNQLRKEGTAIVYISHKLAEIRRICDRYTVM
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BYFLTTNNITQIFVQSSVTVLIGMGEFFAILVAGIDLSVGAILALSGMVTAKLMLAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard_name="REP; repetitive extragenic palindromic

    1. .1885
    /note="1885 bp overlap with end of GenBank Accession
Number U00006 (ECOWU89)"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<1...398)
/note="ORF_f326 of GenBank Accession Number U00006
(ECOWU89)"
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/note="predicted bend of 73.22 degrees"
complement(3030. .3953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     809. .931
/note="predicted bend of 74.75 degrees"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277. .397
/note="predicted bend of 75.10 degrees"
complement(377. .1909)
/note="ORP_f510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains 1 REP sequence" complement (2036. .2971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="predicted bend of 75.87
/note="predicted bend of 75.87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       flh-regulated promoter" complement (1985. .2021)
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/transl_table=11
/label=ORF_f311
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/label=ORF f510
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205073 GITCAGGACGAACACGCACGTITACACTCGAAAAACGCCACAACGGAITGTGGTGCTG 205014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204713 GGCGAAATGGTGGGTAAAAAGCGAGAGATGCAGGACGTCTGGAACAACATAAAGAGAGG 204654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204653 AIGGCGCAGTCAGCCAGCCAGCCAG----CTTCCCAAAGGACACACGCGTGGCCTTTGGCACA 204600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MMGKLIWLMGPSGSGKDSLLAELRLREGTQLLVAHRYITRDASA
GSENHIALSEQEFFTRAGQNLLALSWHANGLYYGVGVEIDLWLHAGFPVLVNGSRAHL
PQARARYQSALLPVCLQVSPEILRQRLENRGRENASEINARLARAARYTPQDCHTLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204449 CIGCIGGITGCCCACTATCGC-----GAAGAGAGCATTGTTAAACGCTGGCAACAA 204399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 ileAlaAspAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThr 144
                   /gene="phnN"
/note="HisP-like nucleotide binding protein (ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIle 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 SerLysalaLeuGlytysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 AspAsnLysLysAsnArgileIleLysProLeuArgAspLysIleGlyLysTyrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||||
204953 GATAACGATGCAAAAGCATCCTGCCCGAAGTGCGTGCGCACCTGAAACCGTGGCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys
                                                                                                                                                                                                                                                                                                                                                  338534
100
62
104
16
                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                   DGSLRQSVDTLLTLIHQKEKHHACL.
complement (7010. .8146)
/gene="phnM"
complement (7010. .8146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-338534)
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  complement (6453. .7010)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-724-972A-6352 (1-335) x ECOUW93
                                                                                                                                                                                                                                                                                                                                             9.21e-23
460.00
57.45%
35.46%
27.22%
                                                           protein) "
                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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VELAKKNGAKIICITHSYHSPIAKLADYIICSPAPETPLLGRNASARILQLTLLDAFF
COMDlement (3952. 3979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (4520. .16191)
/note="corresponds to GenBank Accession Number D90227
(ECOPHN) 1. .11672; the related sequence GenBank Accession
Number J05260 (ECOPHNAQ) is from E. coli B, not K-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MKKIAFGCDHVGFILKHEIVAHLVERGVEVIDKGTWSSERTDYP HYSQVALAVAGGEVDGGILICGTGVGISJANKFAGIRAVVCSEPYSAQLSRQHNDT NVLAFGSRVVUGLELAKNIVDAMLGAQYEGGRHQQRVEAITAIEQRRN" complement (4520. .16191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFNDAITLIDAGLHDIADEMBEGSFQOFLLTHYHMDHVQGLFPLRWGVGDPIPVYGPP
DEQGCDDLFKHPGLLDFSHTVEPFVVFDLQGLOVTPLPLNHSKLTFGYLLETAHSRVA
WLSDTAGLPEKTLKFLRNNQPQVMVMDCSHPPRADAPRNHCDLNTVLALNQVIRSPRV
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Besudomonadacea; Pseudomonas.

1 (bases to 312839)
Busli,(C.R., Joardar,V., Lindeberg,M., Selengut,J., Paulsen,I.T.,
Gwinn,M.L., Dodson,R.J., Deboy,R.T., Durkin,A.S., Kolonay,J.F.,
Madupu,R., Daugherty,S., Brinkac,L., Beanan,M.J., Haft,D.H.,
Khouri,H., Fedorova,N., Tran,B., Russell,D. Berry,K.,
Utterback,T., Van Aken,S.E., Feldblyum,T.V., D'Ascenzo,M.,
Utterback,T., Van Aken,S.E., Feldblyum,T.V., D'Ascenzo,M.,
Deng,W.L., Ramos,A.R., Alfano,J.R., Cartinhour,S., Chatterjee,A.K.,
Delaney,T.P., Lazarowitz,S.G., Martin,G.B., Schneider,D.J.,
Tang,X., Bender,C.L., White,O., Fraser,C.M. and Collmer,A.
The complete genome sequence of the Arabidopsis and tomato pathogen
Pseudomonas syringae pv. tomato DC300, 108, 10181-10186 (2003)
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204398 GATCCGCTCTGGCAGTGTTAACCGCCGCGCAGAGCAGCAGCTGGTTCGGTCGACAGT 204339
                                                                                                                                                                                                                                                                                         312839 bp DNA linear BCT 09-OCT-2003 pv. tomato gtr. DC3000 section 3 of 21 of the
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                                                                                                                                                                                                                                       323
                                                      Aspproval TrpLysLysLeuAsnAlaValLysAsnGinArgValAsplleLeuAspArg 303
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Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
1.312839
                                                                                                                                                                                                                                       AspleuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuVal
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AE016858 AE016853
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                                                                                                                                                                                                                                                             304
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KEYWORDS
SOURCE
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AE016858/c
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JOURNAL
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AUTHORS
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AUTHORS
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63 108 51

Conservative: Mismatches: Indels: Gaps:

5858 (1-312839)

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	QGSDAYLORGARAACULPUTRKDARAS AND TRENK LPGELARS YQGGATCLSVLTDVDFF QGSDAYLORGARAACULPUTRKDF TO THE TOTAL TOTAL THE TOTAL	à	60 ArgValValLeuGluTvrS
	RIVITESGIFNRADVELMEINDVYSFLVGBAFMRAEQPGAELQRLFFPERKPAGGPA Vn"	qq	164288 CGCGTGGTACTGGAATTTT
gene	6415. 7110	ò	80 ValGlvIleAlaAcadenacat
CDS	/ IOCUB_cag="PSPTO0595" 64157110	i á	
	/locus tag="PSPT00595" /note="similar to GP:0050506. idontified https://note="similar to GP:0050506.	g n	
	similarity; putative"	à	100 GlyLysTyrThrSerValGlyTi
	/codon grant=1 /transl_table=11	q	: \{
•	/product="conserved hypothetical protein" /protein id="aa054137 1"	ò	120 LysProAspLeuIleIleAlaA
	/db_xref="G1:28851059"	£	
	/translation="MQDSIIDICVEQGLQAEQDLLASVCSGASGHGLLLMRPSDRALV MPRRMSRLPGFTEASETLADNRMPVLLRFTGGRPVPOSCATVN1111VVAACDAATTON	3 8	
	RIETAVLRLCQPILDLLIELGGKASLGEVAGAELTAVALEGRKAVQTAQRARQSQ GGTRDVVI AUCH I I DEBURMAN AUTHERNA CHENNALEGRKAVQTAQRARQSQ	ò	140 LysileAlaProThrileGluLe ::: ::
	RLAQAYRRLLADL"	d	164048 AGCCTGGCTCCGACGCTGATGTT
gene	complement(71227766) /gene="crp"	ò	160 AlaPheLysThrileSerLysAl
CDS	/locus_tag="PSPTO0596" complement(7122 7766)	q ₀	163988 TCTGCCGGGCTGATCGGCATGGC
	/gene="crp"	ò	180 GluHisAspLvsLvsIleGluGl
	/	අු	163928 GAAAACCGTCAGCACCTGAAAC
	/product="catabolite gene activator Crp"	غ	
	/protein_id="AAOS4138.1" /db_xref="G1:28851060"	3 1	
	/translation="MVAISFTPKANGLDKLLPHAERRRCPAKTNIISAGDRSBSLFFI	g	163874 GTGCTGTTCGGCGTTGCCCGTGA
	DAGIVIVILEDDEKKEMIVALLANNGDFFGELGLFEQPGHESVRSAWVRAKTECEVAET PYETFRELTRKDPEILYAIGSQMAERLRNTTRKVGDLAFLDVTGRVARTILLDLCKQPD	λŏ	220 GlyGlnPheLeuSerGlnLeuGl
gene	AMIHPDGMQIKITRQEIGRIVGCSREMVGRVLKALEEQSLVNVKGKTMVVYGTR" 79768398	д	163814 GGCAGCGTGCTGCAAGCCATCGG
	/locus_tag="PSPT00597" 79768398	ò	240 LeuSerLysTyrLeuLysGlyPr
	/locus_tag="PSPTO0597" /note="identified by match to PPAM protein family HWM	q	:::
	PP02566" 'Codon start=1	ζō	254GluThrieuserGlnVa
	/trans1_table=11 /product="OsmC/Ohr family protein"	qq	163742 AGCCTGGAGCAACTGCTCGCCCT
	/protein_id="AAO54139.1" /db_xref="GI:28851061"	à	272 SerSerAsnGluProSerLeuLy
	/translation="MKARIQWAGEAMFLGESGSGHVVVMDGPPESGGRNLGVRPMEMV LIGLGGCSNYDVVSILKKSRQPIESCEAFLEAERADEDPKVFTKIHLHFVVKGRGIKE	qq	163694 CATTATCGTCGCCCGAGCATTGT
gene	AQVKRAIELSAEKYCSASIMLGNAGVEITHDYEIVELG" 86419435	δ	8
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Length: Matches:

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                                                   AsnSerSerAsnSerSerLysGluSerSerLysAsp 41
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  GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp
                                          85 AspAsnLysLysAsnArglleIleLysProLeuArgAspLysIleGlyLysTyrThrSer
                                                       145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIle
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                15886 ACAAATGAAGGAACCGAAGGCCTTTTGGAACTCGGAATCAAACCTGTGGGGTGCAGTCAAA
                                                                                              16006 ATCGGACTCGAAGGCGAACGAATATCGAAGCGTTGCCGAGCTGAAGCCTGAATTTAATC
                                                                                                                            IleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThr
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 TTCTCCTCTAC 16007	GluGluHisAspLysLys 184	::: GAAGATTTCGATAAAAAA 16067	LysValLeuPro 202	::: CGGGTGTCGGTAATCAGA 16127	SerTyrValGlyGlnPhe 222	::: TCTTTCCCGGGAATTATC 16181	LeuSerAsp 234	 CTGTTTGAGAAACAAGAC 16241	LeuGlnMetAsnThrGlu 254		AsnLysAlaSerSerAsn 274	::: TATAAACCTGCCGAA 16331	LysAspProValTrp 287		AspargaspleuTrpala 307	 BACGATGCGATCTGGACG 16445		
::: ::: ::: 15957 GTCTTCTGAAAGGCTGCGGCGAATGGAAAGACA	SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeu	GCGAAAGCGGTAAACAAAGGGGAAAAGGCCAAAGAAGTTTTAGAAGATTTCGATAAAAA	IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuPro 202		AlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe		LeuSerGlnLeuGlyPheLysGluAla	 TGGATCAGCTCGGATTCAAGTATCCGGAAAAACAGGAAAAACTGTTTGAGAAACAAGAC 16241	AspValThrLysGlyLeuSerLysTyr	GAC			เอ	AGCAAAAAAGAAGCTGAAACATGGCAAAACGATTGGACAAGCGATCCGCTGTGG	LysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeu		308 ArgSerArgGlyLeu 312	16446 ACGCCGCCGCGTA 16460
15957	165	16008	185	16068	203	16128	223	16182	235	16242	255	16275	275	16332	288	16386	308	16446
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A851822 Staphyloc
A851812 Staphyloc
A851812 Staphyloc
ABL15015 Pathogen
Ac20079 Prokaryot
AC74415 Staphyloc
AC40834 Staphyloc
AC40838 Staphyloc
AA183786 DNA
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                         nucleic search, using frame_plus_p2n model
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Searched:

0.5 0.5 7.0

BLOSUM62 Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext

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Sequence:

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SUMMARIES

Query Match Length DB

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geneseqn2004as:* geneseqn2004bs:* geneseqn2003ds:* geneseqn2003cs: genesegn2002bs:* genesegn2003as:* genesegn2003bs:*

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geneseqn1980s: * Geneseq_16Dec04:*

Database :

ADS03285 ACA47084 AAS54519 ACC48532 ACA19774

1008 993 1014 2981 984

100.0 98.9 73.5 73.0

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The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidemidis polypeptide with any cc of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as correct of in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); vector; a cell comprising a recombinant expression vector of (1); vector; a cell comprising a polypeptide; an isolated nucleic acid (1); vaccine composition for prevention or treatment of an S. epidermidis or infection, comprising a nucleic acid cited above and a carrier; treating a subject for S. epidermidis infection; a subject for S. epidermidis infection; a computer of an S. epidermidis of the sequence of a subject for S. epidermidis infection; a computer readable medium having recorded in it the nucleotide sample; a computer readable medium having recorded in it the nucleotide sample; a computer readable medium having recorded in it the nucleotide system for identifying fragments of the Staphylococcus genome of commercially importance; a computer based system for identifying fragments of commercially important nucleic acid fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids of commercially important nucleic acid fragments of the staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcus procession of the invention. This sequence encodes a S. epidermidis protein of the invention.
                                                                                                                       New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1008 BP; 404 A; 129 C; 188 G; 287 T; 0 U; 0 Other;
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Query Match:
DB:
Doucette-Stamm L,
                                                                              P-PSDB; ADS07057
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1008 335 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:

US-10-724-972A-6352 (1-335) x ADS03285 (1-1008)

LysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluileSerLysLeuLys 120 180 240 100 300 360 80 21 IlealarhralaalaCysGlyAsnAsnSerSerSerAsnSerSerLysGluSerSerLys 40 9 9 AspGlyvalGlulleLysHisGluGluGlyThrThrLysValProLysHisProLysArg GlyIleAlaAspAspAsnLysLysAsnArgIleIleLysProLeuArgAspLysIleGly GlyvalGluServalArgGlyLeuLyslleLeuSerVallleGlyLeuLeuPheValLeu 61 41 61 181 81 241 301 121 101 유 g ð 셤 ò 윱 유 ò ò ò à

320 LeugluLysAspProValTrpLysLeuAsnAlaValLysAsnGlnArgValAspIle 300 900 260 780 261 ProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu 280 840 240 900 220 9 160 480 180 540 200 121 ProAspLeullelleAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLys 140 LeuaspargaspLeuTrpAlaargSerArgGlyLeulleSerSerGluGluMetAlaLys PhelyeThrileSerLysAlaLeuGlyLysGluGluGluGluGlyRysArgLeuGluGlu LeuproalavalalaalaalaaserGlyLeuLeualahisProSerAsnSerTyrValGly GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 421 ÁTTGCTCCTÁCGÁTTGAÁCTGAÁAAGTTTCGATGGAGATTATAATGAAAATATTGATGCT 141 IleAlaProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAla HisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysVal Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene. GluLeuValGluLeuSerLysLysAspSerLysLysBysAspAsnLys 335 Prokaryotic essential gene #28741. 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 ACA47084 standard; DNA; 993 Staphylococcus epidermidis (ELIT-) ELITRA PHARM WO200277183-A2. 19-JUN-2003 03-OCT-2002 ACA47084; 196 841 301 321 201 601 221 661 241 721 781 281 161 181 õ 엄 ò ď g ò a 요 8 ò 음 ò ઠે 셤 ò 셤 à 임 ઠે ò

P-PSDB; ABU43214

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

SEQ ID NO 34954; 1766pp; English. Claim

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) an bost cell containing the vector; (3) an isolated on the polypeptide (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation or that has an activity against a biological pathway for proliferation or that has an activity against a biological pathway or equired for proliferation, or that that inhibits cellular proliferation of an organism acts; (9) manufacturing an activity, against a biological pathway in which a proliferation or the biological correquired for proliferation, or that that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprise proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprises or compound; a sectivity; (11) a culture comprise the compound that inhibits proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecic acids required for cellular proliferation to isolate candidate molecic acids required for proliferation in cells other than S. aureus, S. typhimurium, c. prokaryotic essential genes. Note: The sequence data for this patent did control of c ftp.wipo.int/pub/published_pct_sequences

Other; o n Sequence 993 BP; 398 A; 128 C; 183 G; 284 T; 0

993 331 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 3.44e-152 1671.00 100.00% 100.00% 98.88% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: gnment Scores:

US-10-724-972A-6352 (1-335) x ACA47084 (1-993)

ValArgGlyLeuLysIleLeuSerVallleGlyLeuLeuPheValLeuIleAlaThrAla 24 44 64 AlaCysGlyAsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGlu IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValLeu 25 19 45 121 셤 ઠ a g ò ò

AspAsnLysLysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSer 104 85

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124 144 480 SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184 204 224 244 720 264 780 840 284 304 LeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGlu 324 ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle | IleAlaAspAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThr | IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIle ATTGAACTGAAAAGTTTCGATGGAGATTATAATGAAAATATTGATGCTTTTAAAACAATT AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu LysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMet ProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAsp PhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAsp LeuSerLysLysAspSerLysLysAspAspLys 335 541 24:1 105 301 125 145 421 165 185 481 205 225 661 245 781 265 285 841 305 901 325 961 ò d ò g g ò 8 원 ò g g g ò ò g ઠે ò ద ò a ò 셤 ઠે g

AAS54519 standard; DNA; 1014 (first entry) 13-FEB-2002 AAS54519; RESULT 3

cellular proliferation gene; antibiotic; Staphylococcus aureus DNA for cellular proliferation protein #831. Antisense; ds; prokaryotic antibacterial; drug design.

Staphylococcus aureus. WO200170955-A2.

27-SEP-2001.

84

21-MAR-2001; 2001WO-US009180

21-MAR-2000; 2000US-0191078P

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AATTATACTTCTGTAGGTACACGTAAACAGCCAAACTTAGAGGAAATTAGTAAATTAAAA 378
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TTACAAGAAGATCCAACTTGGAAAAGTTGAACGCAGTTAAAAATAATCGCGTGGATATT
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                                                                                           141 IlealaProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAla
                                                                                                                                                        PhelysThrileSerlysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGlu
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                                               HisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysVal
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                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes coli, Staphylococcus aureus, Salmonala typhi, Klebaiela pneumoniae, coli, Staphylococcus aureus, Salmonala typhi, Klebaiela pneumoniae, consetul for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can tasense nucleic acids of sequence in rational drug discovery programmes. The bused to screen compounds in rational drug discovery programmes. The cantisense nucleic acid sequence is also useful to screen for homologous coloranisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent column part of the printed specification, but was obtained in the first control format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProVal
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                                                                                                                                                                                                                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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239
42
50
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                    SEQ ID NO 8156; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                        Zyskind JW,
         23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257362F.
16-FEB-2001; 2001US-0269308P.
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1242.00
84.89%
72.21%
                                                                                                                                                          Ohlsen KL,
                                                                                                                            ELIT-) ELITRA PHARM INC
                                                                                                                                                                        Xu HH;
                                                                                                                                                                                                        WPI; 2001-611495/70.
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Query Match:
DB:
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Yamamoto RT,
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280 858 300 918

240 738 260

200 618 220 678

160 498 180 558

Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection. (DSQU-) D-SQUARED BIOTECHNOLOGIES Claim 4; Page 53; 62pp; English. 2003-300870/29 WPI; 2003-300870, P-PSDB; ABR41865. Scott DL;

The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA03. To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the siderophoral periodic by periplasmic binding production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain etaphylococcal infection. They can also be used to develop diagnostic авваув

T; 0 U; 0 Other; C; 386 G; 1048 Sequence 2981 BP; 988 A; 559

2981 238 42 51 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 3.36e-109 1233.00 84.59% 71.90% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

US-10-724-972A-6352 (1-335) x ACC48532 (1-2981)

1814 1694 1634 1574 140 100 120 20 40 9 80 21 IleAlaThrAlaAlaCysGlyAsnAsnSerSerSerAsnSerSerLysGluSerSerLys AspGlyValGlu11eLysHisGluGluGlyThrThrLysValProLysHisProLysArg ValvalvalieuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProVal GlylleAlaAspAspAsnLysLysAssnArglleIleLysProLeuArgAspLysIleGly LysTyrThrSerValG1yThrArgLysG1nProAsnLeuG1uG1uI1eSerLysLys ProAspleuileileAlaAspAsnAsnArgHisLysGlyIleTyrLysAspleuAsnLys 1573 ATTGCACCACACATTATCATTAAAGAGTTTTGATGGAGACTACAAAAAAATATTAATTCG н 101 1693 41 61 1753 1633 81 121 141 ઠે g ઠે g ò ద ò g ò g g 셤 ઠે 8 ò

screening

New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

PheLysThrlleSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGlu 180

161

1334 1454 1274 1214 240 |||::::::||| |TACAAGAAGATGCAACATGGAAAAGTTGAATGCAGTTAAAAATAATCGCGTGGATATT 1094 280 GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu SerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsn HisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysVal LeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGly ProGluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu LeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsplle LeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLys Zyskind JW; Xu HH; ds; prokaryotic essential gene; cell proliferation; ¥Ř. Ohlsen P Forsyth P Haselbeck R, Yamamoto R, Malone C, Carr GJ, 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 08-FEB-2002; 2002US-00072851 06-MAR-2002; 2002US-0362699P 21-MAR-2002; 2002WO-US009107 gene (first entry) (ELIT-) ELITRA PHARM INC. DNA; Staphylococcus aureus Zamudio C, Trawick JD, WPI; 2003-029926/02. P-PSDB; ABU15904. ACA19774 standard; drug design; gene. WO200277183-A2 19-JUN-2003 Prokaryotic 03-OCT-2002 Antisense; 1513 1453 1393 1333 1273 261 1213 1153 301 181 201 221 241 281 ACA19774; ņ, Wang Wall RESULT 5 ò 셤 à g ò g ò ď g g ò ò ઠે 유 g ò

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Claim 14; SEQ ID NO 7644; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antiseanse sequences given in the specification where expression the 6213 antiseanse sequences given in the specification where expression of the 6213 antiseanse acid inhibits proliferation of a cell. Also included are:

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC of proliferation at the form cell containing the vector; (3) an isolated polypeptide or its framement whose expression is inhibited by the antisense collypeptide or its framement whose expression is inhibited by the antisense collypeptide; (6) inhibiting cellular cc proliferation, or that has an activity against a biological pathway the grounding and proliferation, or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway the proliferation or that has an activity against a biological pathway the proliferation or that has an activity against a biological pathway in which a proliferation or that inhibits proliferation of an organism acts, (9) maniferation required gene or ties gene required for cellular proliferation of an organism acts, (9) maniferation required gene or ties gene or which each of the strains is present in a culture or collection of compound's activity, (11) a culture comprising strains in which the gene compound that inhibits proceed or a gene on which each of the strains is present in a culture or collection of creatins; or (13) identifying the target of a compound that inhibits the cc compound and that inhibits of collection of creatins; or (13) identifying the target of a compound that inhibits for collection of creating for homologous nucleic acids are useful for collection to solate candidate molecules for rational genes. Note: The activity man of the printed genes to sequence data for this patent discovery programs, or for screening homologous nucleic acids required for proliferation to isolate candidate mol
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240 104 124 360 61 GCTTGTGGGTAATACGGATAATTCAAGTAAAAAAAAAGATCATCAACTAAAGATACTATTTGG 120 64 84 9 25 AlaCysGlyAsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGlu 44 GAGTACTCATTTGCAGATGCATTAGCAGCATTAGACGTTAAACCAGTTGGTATTGGTGAT ASPABNLYSLYSASNAYGIJEIJELYSPYOLGUATGASPLYSIJEGIYLYSTYTTHISER ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle GluTyrSerbheValAspAlaLeuValAlaLeuAspValLysProValGlylleAlaAsp 45 IleLysHisGluGluGlyThrThrysValProLysHisProLysArgValValValLeu ValArgGlyLeuLys1leLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAla US-10-724-972A-6352 (1-335) x ACA19774 (1-984) 105 65 181 241 S 85 301 8 g ò 유 ò 8 음 ò ઠે g ઠે ઠે

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                   145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIle
                              185 ileGluGluTyrLysLysGluileThrMetAspLysAsnGlnLysValLeuProAlaVal
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SerLysTyrLeuLysGlyProTyrLeuGlmMetAsnThrGluThrLeuSerGlnValAsn

English NO 5331; 49pp; 6; SEQ ID Claim

The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus genes of the invention

C; 191 G; 300 T; 0 U; 0 Other; Sequence 1044 BP; 425 A; 128

1044 237 43 51 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: 6.25e-108 1214.00 84.59% 71.60% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB: No.:

US-10-724-972A-6352 (1-335) x ACF74986 (1-1044)

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111 20 ||||||||||| 54 GGAGTGGAACG-ATGAGAGTCTAAACCTTTT-AGTATATTGGGATTAATAGTTGCCTTA GlyvalGluServalArgGlyLeuLys1leLeuSerVallleGlyLeuLeuPheValLeu ~

21 IleAlaThrAlaAlaCysGlyAsnAsnSerSerSerAsnSerSerLysGluSerSerLys 40

AspGlyValGluIleLy8HisGluGluGlYThrLysValProLysHisProLysArg 41

ValvalvalLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProVal 61

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Trawick JD,

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Wall

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Zyskind

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Ohlsen Xu 田;

Haselbeck R, Yamamoto RT,

WPI; 2001-611495/70. P-PSDB; AAU33963 of

New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.

Claim 27; SEQ ID NO 4404; 511pp; English.

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요 요

GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 240

221

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia Coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus facazils. The invention is also useful for the identification of potential new targets for antibiocic development. The antisense nucleic acids can also be used to identify

300 280 831 LeuAspArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLys 320 891 951 ProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu LeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsplle |||::::::||| TTACAAGAAGATGCAACAIGGAAAAGTIGAATGCAGTIAAAAATAATGCGGGGGAIAIT cellular proliferation gene; antibiotic; Staphylococcus aureus DNA for cellular proliferation protein #239 1012 GAACTTGTTGAATTATCAAAAAAGAACAAAAG 1044 331 GlubeuValGlubeuSerbysbysPSerbys 2000US-0191078P. 2000US-0206848P. 2000US-0207727P. 2000US-0242578P. 2000US-0253625P. 2000US-0257931P. 2001US-0269308P. 21-MAR-2001; 2001WO-US009180 927 Antisense; ds; prokaryotic antibacterial; drug design. (first entry) (ELIT-) ELITRA PHARM INC. AAS51822 standard; DNA; Staphylococcus aureus. d8; WO200170955-A2 26-MAY-2000; 23-OCT-2000; 27-NOV-2000; 22-DEC-2000; 13-FEB-2002 21-MAR-2000; 23-MAY-2000; 16-FEB-2001; 27-SEP-2001 Antisense; 261 832 281 301 952 892 321 AAS51822 ò ద ò 엄 ò 셤 δ g

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antibodies capable of binding to the expresse these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes coli, Staphylococcus aureus, Salmonala typhi, Klebbiela pneumoniae, coli, Staphylococcus aureus, Salmonala typhi, Klebbiela pneumoniae, compactives and Enterococcus faccalis. The invention is also pseudomonas aeruginosa and Enterococcus faccalis. The invention is also consecut for the identification of potential new targets for antibiotic compacting used in proliferation, to express these proteins, and to obtain corrections used in proliferation, to expressed proteins, and to obtain contibodies capable of binding to the expressed proteins. The pressence contisense nucleic acid sequence is also useful to screen for homologous antisense nucleic acid sequence encodes an essential prokaryotic of organisms. The present sequence encodes an essential prokaryotic colorganisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent cold not form part of the printed specification, but was obtained in celectronic format directly from WIPO at
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                                                                                         ProSerLeuLysGluLeuGluLysAsproValTrpLysLysLeuAsnAlaValLysAsn
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drug design.
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ftp.wipo.int/pub/published_pct_sequences

Alignment Scores 용 114 174 105 GlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIle 125 354 126 AlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLyslleAlaProThrlle 145 414 474 LysalaleuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLysIle 185 234 294 GluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSer 165 69 45 65 226 LeuglyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLys 245 85 654 GlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe 265 Pro---ValTrpLysLysLudsnAlavalLysAsnGlnArgValAspIleLeuAspArg 303 266 IleMetThrAsn---LysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAsp 284 86 AsnLysLysAsnArgileilelysProLeuArgAspLysIleGlyLysTyrThrSerVal 235 GGCAGCAGTAAAAATATAACAAAGTCAGTAAGAGATAAGGGTTGGGGCATATGAATCGGTT ArgGlyLeuLys1leLeuServal1leGlyLeuLeuPheValLeuIleAlaThrAlaAla СуяGlyAвпAвпSerSerAвпSerSerLysGluSerSerLysAspGlyValGluIle ||||||| | TGTGGTCAAAAGATACT------GAAGAGAAAACTGAAATGACGACAATA LysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGlu 295 GGATCTAGACCGCACCGAATATGGAAGTGATAAATTAAAATCGGATTTGATCATA ::::::|||||||||||||||::: GluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAla 535 GCGGAGATTAGAAAGAAAATTGAACAGAGTACGTTAAAAACTGCATTTGCATTCGGTATC AlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGln U; 0 Other; 957 153 61 99 12 Length:
Matches:
Conservative:
Mismatches:
Indels: 0 .. Sequence 957 BP; 382 A; 114 C; 209 G; 252 US-10-724-972A-6352 (1-335) x AAS51612 (1-957) 726.00 65.85% 47.08% 42.96% Percent Similarity: Best Local Similarity: Scores 56 46 901 655 355 146 415 166 475 186 506 246 715 Query Match: DB: 823 Score: SXS 셤 ઠે g ઠે ò a 8 a ò g ઠે g ઠે 셤 ò g g ሯ 8 6 8 6 8 6 g ઠે ઠે 셤 ò

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coll, Staphylococcus aureus, Salmonella typhi, Klebbiella pneumoniae, coll, Staphylococcus aureus, Salmonella typhi, Klebbiella pneumoniae, con seful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify noteins used in proliferation, to express these proteins, and to obtain antisense nucleic acids equence is also useful to screen for homologous con used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous colorganisms. The present sequence encodes an essential prokaryotic collular proliferation protein. Note: The sequence data for this parent collular proliferation protein. Note: The sequence data for this parent collular proliferation protein. Note: The sequence data for this parent collular proliferation protein. Note: The sequence data for this parent collular proliferation protein. Note: The sequence data for this parent collular proliferation protein. Note: The sequence data for this parent collular proliferation protein. Note: The sequence data for this parent collup. Note: The sequence collup. Note: The sequence data for this parent collup. Note: The sequence sea obtained in the wind proliferation int/pub/published_pot_sequences
                      AspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuVal 323
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                                                                                                                                                                                                                                                                                                                                                    Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                             Staphylococcus aureus DNA for cellular proliferation protein #699.
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Xu HH;
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23-MAY-2000; 2000US-0206848P.
23-OCT-2000; 2000US-020727P.
23-OCT-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-025931P.
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                                                                                                                                                                                            AAS54387 standard; DNA; 960
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                  943 AAAATTGCAGAAAAA
                                                                         GluLeuSerLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus
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Yamamoto RT,
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304
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pro---valirpLysLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCAGCAGTAAAAATATAACAAAGTCAGTAAGAGATAAGGTTGGGGCATATGAATCGGTT 288
                                                                                                                                                                                                                                                                                                                     AlaAspAsnAsnArgHisLy8Gly1leTyrLysAspLeuAsnLysIleAlaProThrile 145
                                                                                                                                                                                                                                                                                                                                                            GluLeuLysSerPheAspGlyAspTyrAsnGluAsnileAspAlaPheLysThrIleSer 165
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TTAGCCACTGACGGAAAAACGGACAAAATAGAACGAAATTC-----ATTGAT
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TCAAGAGCAGGTATGTTAATAATGAAGATACATTTATGGGACAATTCTTAAA
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                                                                                         ArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAlaAla
                                                                                                                                                                              LysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGlu
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                                                                                                                                                                                                                      TyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAsp
                                                                                                        CysGlyAsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGlulle
960
153
61
99
12
 Length:
Matches:
Conservative:
Mismatches:
                                          Indels:
Gaps:
                                                                         US-10-724-972A-6352 (1-335) x AAS54387 (1-960)
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726.00
65.85%
47.08%
42.96%
                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, producing hyperimmune serum-reactive antigens from a pathogen, a tissue or host prone to auto-immunity, where the antigens are coordine, comprises providing antibody preparation from a plasma to pool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the coordination to their hyperimmune serum-reactive antigens comprising any of the immunity. The hyperimmune serum-reactive antigens comprising any of the correction preparation, particularly a vaccine against staphylococcal pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The corrections or colonisation caused for diagnostic and imaging purposes. Other conditions may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral companies in the polynucleotide sequence represents staphylococcal DNA relating to the method for identifying and producing pathogen specific antigens of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying, isolating and producing hyperimmune serum-reactive antigen
from a pathogen, for preparing vaccine or medicament for treating or
preventing e.g. staphylococcal infections, comprises providing antibody
                                                                                                                                                                                                                                                            Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis; gene; ds.
                                                                                                                                                                                                                        Pathogen specific antigen related staphylococcal DNA SEQ ID No 301.
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Hafner P
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Etz H, Dryla A, Weichhart T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2002; 2002WO-EP000546.
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324 GluLeuSerLysLys 328
                                      951
                                                                                                                ABT15015 standard; DNA; 957
                                                                                                                                                                                              (first entry)
                        937 AAAATTGCAGAAAAA
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Minh DB, Vytvytska O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-075410/07.
                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus sp.
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                                                                                                                                                          ABT15015;
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U; 0 Other;

T; 0

210 G; 248

383 A; 116 C;

Sequence 957 BP;

invention

Alignment Scores:

957 149 63 95 11

Conservative: Mismatches: Indels:

1.34e-60 724.50 66.67% 46.86% 42.87%

Best Local Similarity:

Query Match:

Percent Similarity

prokaryotic essential gene; cell proliferation;

21-MAR-2002; 2002WO-US009107

gene #1736

Prokaryotic essential

Antisense, da; prok drug design; gene.

Staphylococcus aureus.

WO200277183-A2.

03-OCT-2002.

(first entry)

19-JUN-2003

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                       212
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                                    AsnSerSerLysGluSerSerLysAspGlyValGluileLysHisGluGluGlyThrThr
                                                                            73 ValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLysAsnArgIleIle
                                                                                                                                         ThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAla
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                                    33
                13
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                                                                                                                                                                                                                                                                                                                                           868
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ACA20079
ID ACA20
XX
ACA20
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

mucleic acid; (2) a host expression is inhibited by the antisense

conciding a polypeptide whose expression is inhibited by the antisense

conciding a polypeptide (5) production the polypeptide; (6) inhibiting cellular

concideration or the activity of a gene in an operon required for

proliferation or the activity of a gene in an operon required for

proliferation or that has an activity against a balological pathway

concidentifying a gene required for cellular proliferation; (8)

defentifying a gene required for cellular proliferation or the biological

compound a proliferation-required gene or its gene product is

compound a activity; (11) a culture comprising strains in which the gene

compound s activity; (11) a culture comprising strains in which the gene

compound s activity; (11) a culture comprising strains in which the gene

compound s activity; (11) a culture comprising strains in which the gene

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compound s activity; (11) a culture comprising strains in which the gene

compound s activity; (11) a culture comprising strains in which the gene

compound s activity; (11) a culture comprising strains in which the gene

compound s activity; (11) a culture comprising strains in which the gene

compound so or each of the strains is present in a culture or collection of

compound so or each of an organism. The antisense nucleic acids required

confideration of an organism. The antisense nucleic acids required

confideration of an organism. The present sequence is one of the target or proliferation to isolate candidate molecules for retional drug discovery programs, or for screening for molecules of the printing and profice sesential gene or servents
                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                   Zyskind X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Forsyth |
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 7949; 1766pp; English.
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Carr GJ,
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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P-PSDB; ABU16209.
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Wall D,
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960

Length: Matches:

standard; DNA; 960

ACA20079 ACA20079

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ACF74415 standard; DNA; 975
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                                                                                                                                                                                                                                                                                                                        AspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGlu 172
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                                                                  ValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsnAsnSerSerSer
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      Conservative:
             Mismatches:
Indels:
Gaps:
                                                  (1-335) x ACA20079 (1-960)
      66.67%
46.86%
42.87%
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Query Match:
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The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 AsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGluGluGlyThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wew scapnylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VallleGlyLeuLeuPheValLeulleAlaThrAlaAlaCysGlyAsnAsnSerSerSer
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Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful producing antibodies effective against Staphylococci infection.

(DSQU-) D-SQUARED BIOTECHNOLOGIES INC

WPI; 2003-300870/29

Scott

P-PSDB; ABR41867

17-JUN-2002; 2002WO-US019224 17-JUN-2001; 2001US-0298975P

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|GATTATAATGCAAATATTGAAGCATTTAAAACAGTCGCTAAAGCAGTAGGCAAAGAGAAA
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                                                                                                                                                                                                                         The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA05. To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and functional domains. The SEIP encoded from clones expressing SEIPs, and functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, for combination, to produce anti-staphylococcal antibodies used individually, or passive or active immunisation strategies to prevent or contain stabhylococcal infection. They can also be used to develop diagnostic
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                                                                                                                                                                               ThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsn---LysAla 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a novel polypeptide, which is optionally expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding it, are derived from Staphylococcus aureus. Cells expressing ligands binding the polypeptide can be used to isolated candidate compounds that
                                                                                                                                                                                                                                       GACAAAAATAGAACGAAATTC------ATTGATCCTGCAGTTTGGAAATCATTA
                                                                                                                                                                                                                                                                     1838 AAAGCTGTGAAAGATAAAAGTTTATGACGTTGACCGAAATAAGTGGTTGAAATCAAGG
LSSO GAACAGAGTACGTTAAAATCTGCATTTGCATTCGGTATCTCAAGAGCAGGTATGTTTATT
                                                                                                                                           SerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Staphylococcus aureus polynucleotide and polypeptide(s) - for isolating antagonist of the polypeptide(s) useful as anti-bacterials
                                                                 193 ThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAla
                                                                                                     Hi8ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeu
                             GluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIle
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                                                                                                                                                                                                                                                                                                         GlyLeuIleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLys 328
                                                                                                                                                                                                                                                                                                                                                                                                              encoding cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bind and inhibit the activity of the polypeptide. Such compounds can be used as anti-bacterial compounds. The polypeptide may also be used as immunogen to vaccinate an animal for protection against Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeulysProAspleuileileAlaAspAsnAsnArgHisLysGlyileTyrLysAspleu
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169
36
69
9
                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                 Sequence 2247 BP; 704 A; 397 C; 307 G; 802
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721.00
73.48%
60.57%
                                             caused disease
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Best Local Similarity:
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Pred. No.:
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::: CTTTTAGTTGCAGCTTGTGGTAATACGGATAATTCAAGTAAAAGAAGAAGAATCATCAACTAA 712

sAspGlyVal-GluIleLysHisGluGluGlyThrLysValProLysHisProLysA

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771 40

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21 IleAlaThrAlaAlaCysGlyAsnAsnSerSerSerAsn-SerSerLysGluSerSerLy rgvalvalvalleuglufyrserPhevalAspAla---LeuvalAlaLeuAspvalLysP

99 IleGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLys

ro-ValGlyileAlaAspAspAsnLysLysAspArgileIleLysProLeuArgAspLys

356

296

AspAlaPheLys-ThrileSerLysAlaLeuGlyLysGluGluGluGluGlyLysLysArgLe 178

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414 GCCCACATTGCACCACA TIATCATTAAAGAGTTTTGATGAGAGACTACACCCACAATATT

uGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGl 198

nLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTy

235 CAAAGTGCTTCCAGCAGTAGTTGCTAAAGCTGGTTATTAGCACATCCACACTATTCATA 176

rValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLy 238

sGlyieuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGl 258

238 115

218 175

TO /21-7/28-0332.FDG

BP. AAT83786 standard; DNA; 2247 AAT83786 AAT83786/c

(first entry) 16-JUL-1998

encoding 3 Staphylococcus aureus proteins of unknown function. NA V

Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome; toxic shock syndrome; ss.

Staphylococcus aureus.

complement (1456. .1587) complement(1212. .1445) Location/Qualifiers CDS

/*tag= b complement(1705. .2016) /*tag= c

WO9730070-A1

21-AUG-1997

97WO-US002318.

96US-0011888P 20-FEB-1996;

SMIK) SMITHKLINE BEECHAM CORP.

Nicholas RO; Knowles DJC, Ward JM; Hodgson JE, Kr Rosenberg M, Burnham MK, Reichard RW, Black MT, Pratt JM,

WPI; 1997-424969/39

P-PSDB; AAW27819, AAW27820, AAW27821

10 Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used isolate antimicrobial compounds, and in vaccines against S. aureus infection.

Claim 9; Page 672-673; 989pp; English.

The present sequence encodes 3 Staphylococcus aureus proteins of unknown function. The present sequence was isolated from a library of clones of S. aureus WCHM 29 in Escharichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. sureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock

Sequence 2247 BP; 704 A; 397 C; 307 G; 802 T; 0 U; 37 Other;

Length: Matches: Conservative: Mismatches: Indels: Gaps: 8.49e-60 721.00 73.48% 60.57% Percent Similarity: Best Local Similarity: .gnment Scores: Query Match:

2247 169 36 69 9

US-10-724-972A-6352 (1-335) x AAT83786 (1-2247)

GlyValGluSerValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeu 20

Bacillus subtilis strain MB1510 integration region DNA SEQ ID NO:20. nValAsnProGluArgMetPhelleMetThrAsnLysAlaSerSerAsn 274 expression library; Gram-positive bacterium host cell; non-replicating linear integration cassette; gene; Bacillus; BP. ADF30765 standard; DNA; 5718 12-FEB-2004 (first entry) Bacillus subtilis 258 55 ADF30765 ADF30765/C
ADF30765/C
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AC ADF30
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DT 12-FE
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20-NOV-2003

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Generating an expression library of polynuclectides by introducing the linear integration cassette into the host cell and selecting or screening for host cells that produce the polypeptides of interest.
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PK;
                                                                                          Hansen
07-MAY-2003; 2003WO-DK000301
                            07-MAY-2002; 2002DK-0000682
                                                                                          Jorgensen PL,
                                                            (NOVO ) NOVOZYMES AS
                                                                                            Bjornvad ME,
```

WPI; 2004-012127/01.

gxample 5; SEQ ID NO 20; 55pp; English.

The present invention describes a method for generating an expression to the present invention describes a method for generating an expression of the genome of a competent Gram-positive bacterium host cell. The method to the genome of a competent Gram-positive bacterium host cell. The method comprises: (a) providing a non-replicating linear integration cassette; and (b) introducing the linear integration cassette into the host cell and selecting or screening for host cells that produce the polypeptides of interest; (b) a 5' flanking polynucleotide encoding one or of interest. The cassette comprises: (a) a polynucleotide segment comprises of the polynucleotide of the segment comprising a first homologous region located in the 3' end of the segment; and (c) a 3' flanking comprising a second homologous region located in the 5' end of the polynucleotide segment downstream of the polynucleotide of (1) and comprising a second homologous region located in the 5' end of the segment. The first and second homologous regions are at least 50', 1000 esement. The first and second homologous regions are at least 80, 85, 90 or 1500 bp, each of which has a sequence identity of at least 80, 85, 90 or 1500 bp, each of which has a sequence identity of at least 80, 85, 90 or 1500 bp, each of producing a polypeptide of interest. The method is useful (2) a method of producing a polypeptide of interest. The method is useful consequence recombination into the genome of a competent Gram-positive bacterium host cell. The present sequence represents a Bacillus subtilis subtilis subtilis subtilis integrated. present invention.

C; 1259 G; 1677 T; 0 U; 0 Other; Sequence 5718 BP; 1693 A; 1089

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5718
149
50
103
15
     Length:
Matches:
Conservative:
                              Mismatches:
Indels:
      2.84e-55
679.50
62.78%
47.00%
                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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US-10-724-972A-6352 (1-335) x ADF30765 (1-5718)

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                                        AsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGlulleLysHis 47
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LeuLysileLeuServalileGlyLeuLeuPhevalLeulleAlaThrAlaAlaCysGly 27
                                                                                                                                          PheValAsphlaLeuValAlaLeuAspValLySProValGlyIleAlaAspAspAsnLys
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                                                                                                                                                                                    SerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGly
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                             AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu
                                                                   LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla
                                                                               308 ArgserArgGlyLeulleserSerGluGluMetAlaLysGluLeuValGlu 324
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TTTACACACGCTGTGAAGTCAGAT-----T
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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241 GGGGTTGCTGATGACAACAAACCAAATCGTATTATTAAAACCATTAAAAGAAAAATTGGA 300

101 LysTyrThrServalGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLys

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ž Forsyth RA, Yamamoto R, 3 Carr Trawick JD, WPI; 2003-029926/02. P-PSDB; ABU43367. ò Wall

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Claim 14; SEQ ID NO 35107; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression to the 6213 antisense sequences given in the specification where expression (1) a vector compitaing a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an best cell containing the vector; (3) an isolated of antisense nucleic acid; (4) an antibody capable of specifically binding collypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or tis gene product lies or a gene on which the test compound that inhibits proliferation of an compound sactivity; (11) a culture comprising strains in which the extent or operation of an account of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candigues mucleic acids required for proliferation in cells of a compound that inhibits the control are proliferation to isolate candidate molecules for rational required for proliferation in cells of the than S. autenus, s. typhimmrium, cells required for proliferation in cells of the printed specification, but was obtained in the printed for proliferation to isolate candidate. So the proper of the printed specification, but was obtained in the cell o

Sequence 525 BP; 200 A; 66 C; 96 G; 163 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: 3.91e-53 644.00 84.00% 70.86% 38.11% Percent Similarity: Best Local Similarity: Query Match: DB:

521 224 44 44 14

US-10-724-972A-6352 (1-335) x ACA47237 (1-525)

61 GCTTGTGGTAATGTTAGCAATAATGGATCAGGTGATTCAGGTAATAAATCGTCATCGAAA 120 5 ValArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeulleAlaThrAla 24 AlaCysGlyAsnAsnSerSerSerAsnSer-----SerLysGluSerSerLys 40 25 용 ઠે ò g

AspGlyValGluIleLysHisGluGluGlyThrThrLysValProLysHisProLysArg 60

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GlyIlealaAspAspAsnLysLysAsnarglleIleLysProLeuArgAspLysIleGly 100 81

301 GATTATAAATCTGTTGGTGCTCGTAAACAACCCAACTTAGAAGAAATCAGTAAATTAAAA 360 ProAspLeullelleAlaAspAsnArgHisLysGlyIleTyrLysAspLeuAsnLys 140 IleAlaProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAla 160 Zyskind JW; Xu HH; ds; prokaryotic essential gene; cell proliferation; Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA, Prokaryotic essential gene #24493. Malone C, Carr GJ, ACA42836 standard; DNA; 897 BP. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 19-JUN-2003 (first entry) (ELIT-) ELITRA PHARM INC. Pasteurella multocida. Zamudio C, Trawick JD, drug design; gene WO200277183-A2 21-MAR-2001; 03-OCT-2002 Antisense; 121 141 ACA42836; ijĠ RESULT 18 Wang Wall ACA42836 DP. δ 셤 유 8 ò

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. WPI; 2003-029926/02. P-PSDB; ABU38966,

Claim 14; SEQ ID NO 30706; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular continuation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway continued for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological

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ProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu 281 LeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIle 742 TGGGAAAATGAAGCCTTATGGAAAATTATCCCTGCGGTAAAAAATGGTCAAGTCATCTTA 301 LeuAspArgAspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLys

691 261

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802 GCTAATGATAATTTATGGGCAAGAGCACGTGGTATTGATGCCGCTGAAGTAATGGTAAA 861

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corputhway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene of compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidates molecules for rational cardid for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, craduired for proliferation in cells enemered acts for this patent did not form part of the printed specification, but was obtained in clearing trom wird form WIPO at the printed for proliferating from WIPO at the printed process.
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897 1111 65 98 17 Length: Matches: Conservative: Mismatches: Indels: 1.67e-40 516.50 60.48% 38.14% Percent Similarity: Best Local Similarity: gnment Scores: Query Match: DB:

US-10-724-972A-6352 (1-335) x ACA42836 (1-897)

AlaAspAspAsnLysLysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyr 102 driaccorcalagarcalaladoscaltraccriagaraccialaccidalacerteri 126 127 GCCTTAGAATATTCTTATGTGGATGCACTTGCACAAATTGGTGTCAGCCCTGTTGGTGTC 186 82 ValGlulleLygHisGluGluGlyThrThrLysValProLysHisProLysArgValVal ValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlylle ThrservalGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAsp 67 63 187 103 43 83 요 δ 음 ઠ g δ g ò

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LyslysileGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuPro 202 487 CAGGATATTGCGGACATCGCCAAA----ACGTTACCGAAAGGGAAAAAAGCGATTATC 183

AlavalAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe 541 GGTGTTTCACGTGAAACCCAATTTAATTATATAGCGAATCCTATGCTGGTGGCTTA LeuSerGlnLeuGlyPheLys-----GluAlaLeuSerAspAspValThrLysGlyLeu 203 223

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SerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsn

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Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag Bacillus licheniformis genomic sequence tag (GST) #2066. Differential gene expression, genomic sequenced altered culture condition, environmental stress; physiological provocation; ds. 321 GluLeuValGluLeuSerLysLysAspSerLys 331 ||||::: ::||| 862 GAAGTCCAAGACTTTGTAACGAAATCCGCCAAA 894 Claim 4; SEQ ID NO 2066; 200pp; English. BP (NOVO) NOVOZYMES BIOTECH INC. (NOVO) NOVOZYMES AS. 06-OCT-2000; 2000US-00680598. 27-MAR-2001; 2001US-0279526P. 05-OCT-2001; 2001WO-US031437. ABK74775 standard; DNA; 801 (first entry) Bacillus licheniformis Clausen IG; WPI; 2002-416684/44. WO200229113-A2. 13-AUG-2002 11-APR-2002 ABK74775; Berka R, array RESULT 19 **ABK74775** 용

The invention describes a method of monitoring differential expression of a genes in a first Bacillus cell relative to expression of the genes in cher Bacillus cells, comprising hybridising labelled nucleic acid probes cother Bacillus cells to a substrate containing array of Bacillus accommic sequenced tags (GST), examining the array, and determining cellative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of a spot in the array. The method is useful for megenes in a first Bacillus cells. The method is useful for monitoring in one or more second Bacillus cells. The method is useful for monitoring cones, identifying possible functions of unknown open reading frames and connecting gene copy number variation and stability. Monitoring changes continue cells adapt to changes in culture conditions, con with a stression of genes may be used to provide a representation of the way con which Bacillus cells adapt to changes in culture conditions, con without a stress or other physiclogical provocation. Extensive follow cup characterisation is unnecessary, when one spot on an array equals one copen con page of the configuration is available.

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Page
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Antibacterial, fungicide, insecticide, polymorphism, genetic analysis; detection, food, gene expression, plant, animal, microorganism, toxin, antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough; gene; ds.

Photorhabdus luminescens.

WO200294867-A2

28-NOV-2002

Photorhabdus luminescens nucleotide sequence #9357,

(first entry)

20-NOV-2003

ACF70890;

BP.

606

ACF70890 standard; DNA;

72-2/44-0332. FIND

c sequence of Photorhabdus luminescens and encoded polypeptides e.g. as therapeutic antimicrobials and agricultural pesticides

Claim 2; SEQ ID NO 9357; 1205pp; French.

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Frangeul

Glaser P,

Taourit S,

Buchrieser C;

Duchand E.

WPI; 2003-148459/14.

Genomic sequence

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(INSP) INST PASTEUR. (CNRS) CNRS CENT NAT RECH

07-FEB-2002; 2002WO-IB003040 07-FEB-2001; 2001FR-00001659

GlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeu 119 This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences GTCGGAATTGCGGACGACAAACCTAAGTTTATTAACGAGAAAGGTCAGGGGAAAAATC 122 123 AAAGGGTATACTTCAGTCGGTTCGCGCGCCCAGCCAAGCTTTGAAAAATTGCTTCTTA 182 302 419 219 LygProAspLeullelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsn 139 LysileAlaProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAsp 159 GluHisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLys 199 79 62 66 80 ValGlylleAlaAspAspAspAspLysLysAspAspTglleIleLysProLeuArgAspLysIle ArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysPro 200 ValieuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrVal Sequence 801 BP; 257 A; 166 C; 204 G; 174 T; 0 U; 0 Other; 801 108 58 95 3 Length: Matches: Conservative: Mismatches: Indels: Gaps: (1-801)US-10-724-972A-6352 (1-335) x ABK74775 5.54e-40 510.50 62.88% 40.91% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: 63 801 363 120 140 243 160 303 180 8888888 Š 셤 ò 셤 8 g ઠે ద ठे 셤 ઠે g ઠે 8 & B

The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens of control amplification of the genes. Antibodies (Ab) raised against the and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens. e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector and antibiotics produced by P. C. mimals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Luminescens. Cells transformed to express the genes are useful for recommentation of the proteins, particularly toxins and cantibacterials useful as insecticides, bactericides and fungithat care sensitive to P. luminescens and the proteins or fungi that care sensitive to P. luminescens encoded toxins or antibiotics) and as containing the genes and the proteins are as virulence care sensitive to the indirection of the genes and the proteins are as virulence containing the genes and the proteins are as virulence containing the genes and the proteins are as virulence containing the genes and the proteins are as virulence containing the genes and the proteins are as virulence containing the genes and the proteins are as virulence containing the genes and the proteins are as virulence contains and an encoded toxing or antibiotics) and as containing the genes and the proteins are as virulence contains and manual sequence represents one of the isolated P. luminescens genes ACETOR AC 479 239 536 240 LeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnVal 259 LysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgVal 298 :::||| 420 ATTCTTCTGGGGAACACAAATGAAGAAATCACCGTGCGCGATGAAAACTTTTTCACG 220 GlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGly GATGCCGAAAACGGTGAATCGTCATATAAAATGACGCTCGAACAGCTGCTTGAGAAA AsnProGluArgMetPheIleMetThr---AsnLysAlaSerSerAsnGluProSerLeu 537 260 597 279 657

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Sequence 909 BP; 230 A; 258 C; 225 G; 196 T; 0 U; 0 Other; 909 102 60 107 14 Length:
Matches:
Conservative:
Mismatches: 1.42e-36 476.00 57.24% 36.04% 28.17% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

717 TATGAAGCCGACAGATTCGCCTGGTCGCTCCGACGCAGCATTGACGGAGCAGCAGTGAGCTG 776

AlaLysGluLeu 322 ATGGATGAAATC 788

177

AsplleLeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMet

299

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8 6 6 6

(1-909)(1-335) x ACF70890 US-10-724-972A-6352

ValGlulleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValVal 62

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                                                                                                                                                                                                                                                                                       544 GGCACCTCGCGCGAACAGCAATTTAACCTGCACTCCAGCGATACCTATACCGGCAGCGTC 603
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----CATGCGGCAATGGTTTCTCTCAACCTGGAACAGTTACTGGCACTCAATCCTGAC 696
                                                                                                                                                                                                  ThrijeSeriyşAlaLeuGlyty8GluGluGluGlyLy8ty8ArgieuGluGluHi8A8D 182
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                                                                                                                                                                                                                                    LyslyslleglugluTyrLysLysGlulleThrMetAspLysAsnGlnLysValLeuPro 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insecticide protein; transgenic plant; insect-resistant plant; wheat; maize; gene; ds.
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                                                                                                                                          ValleuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIle
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GTAAAAATC 876
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83 AlaAspAspAspAspAspAspAspAspAspIleIleLysProLeuArgAspLysIleGlyLysTyr 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid from Photorhabdus luminescens, useful for producing insecticidal polypeptides active against Lepidoptera, and for producing insect resistant transgenic plants.
                                                                                    21345. .22598
/*tag= b
/product= "Photorhabdus luminescens insecticide protein
#2"
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                                               product = "Photorhabdus luminescens insecticide
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102
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Matches:
Conservative:
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AGRONOMIQUE
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ocation/Qualifiers
                    0872. .21306
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476.00
57.24%
36.04%
28.17%
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P-PSDB; ADR20889, ADR20891.
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Qy 143 ProThrIleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLys 162 Db 8207 CCTGTCCTGCTGCTAAATCCCGCAACGAACCTACGAAGAACTCTCCAATCTCCCCGC 8148 Qy 163 ThrIleSerLysAlaLeuGlyLysGluGluGlyLysLysArgLeuGluGluHisAsp 182 Db 8147 ATCATCGGCAAGTCATGGGGAAGGAGTGGAATGCAGAACGGCTGGCAGACCCT 8088 Qy 183 LysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGluUGluHisAsp 182 Db 8087 GAACGCATGAAGGCTATGCCAGAAGAGAGCAGAACGCTGAGAGCACCTTT 8034 Qy 203 AlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGnThrT 8034 Qy 203 AlaValAlaAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe 222 Db 8033 GGCACCTGCGCGCACAGCACTCCAGCACTCCAGCGCACCTCTAGCGCACCTTTTT CGCACACTCAATCCGGCACCCTCTAACCGCCACCACACTTAATCCGGCACACTCAATCCGGCACACTTAATCCGGCACATTAATCCGCACACTTAATATCCGCACAATTAATCATTAATATATAT	Asnalava acagcaca slyLeuil : : :	ACEG7367 39/C Continual (10 of 57) of ACE67367 from base 390001 (Photorhabdus luminescens nucleoti WP Sequence split inc 57 fragments LOCUS ACE67367 Accession Acf67367 WP ACE67367 00 100001 110000 WP ACE67367 01 100001 210000 WP ACE67367 03 300001 210000 WP ACE67367 04 4100001 310000 WP ACE67367 05 500001 310000 WP ACE67367 05 500001 1100000 WP ACE67367 07 100001 1100000 WP ACE67367 07 100001 1100000 WP ACE67367 07 1000001 1100000 WP ACE67367 10 1000001 1100000 WP ACE67367 11 100001 1100000 WP ACE67367 12 1200001 1310000 WP ACE67367 13 1200001 1310000 WP ACE67367 14 1200001 1310000 WP ACE67367 15 1200001 1310000 WP ACE67367 12 1200001 1310000 WP ACE67367 12 1200001 2100000 WP ACE67367 21 2200001 2310000 WP ACE67367 22 2200001 2310000 WP ACE67367 23 2200001 2310000 WP ACE67367 24 2200001 2310000 WP ACE67367 24 2200001 2310000 WP ACE67367 25 2200001 2310000 WP ACE67367 24 2200001 2310000 WP ACE67367 25 2200001 2310000 WP ACE67367 24 2200001 2310000 WP ACE67367 25 2200001 2310000 WP ACE67367 24 2200001 2310000 WP ACE67367 25 2200001 2310000

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                                                                         ThrileSerlysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAsp
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                               ProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLys
                                             ds; prokaryotic essential gene; cell proliferation;
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-0362851P.
06-MAR-2002; 2002US-0362699P.
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                                                                               243 TyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGlu 262
                                                                                                                        ArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGlu 282
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites promiter operated by linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (1) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway confirming a gene required for cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or ties gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts. (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the test compound that inhibits or compound's activity; (11) a culture comprising strains in which the estrain or expension or indicate molecules for rational compound's activity; (11) a culture comprising strains or close or described for proliferation to isolate candidate molecules for rational required for proliferation to isolate candidate molecules for rational required for proliferation in calls order than S. auteurs, s. typhimmrium, confirmed for the printed specification, but was obtained in the printed pot the printed specification, but was obtained in the printed for proliferation or sequences.
                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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             ž
             Forsyth RA,
        Yamamoto R,
                                                                                                                                                                                                                                    Claim 14; SEQ ID NO 19870; 1766pp; English.
     Carr GJ,
  Trawick JD,
                                                    WPI; 2003-029926/02.
P-PSDB; ABU28130.
Wall D,
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U; 0 Other; Length:
Matches:
Conservative:
Mismatches:
Indels: Sequence 900 BP; 198 A; 266 C; 256 G; 180 T; 0 4.95e-35 460.00 57.09% 35.82% 27.22% Alignment Scores:

129 AspAsnLysLysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSer 104 105 ValGlyThrArgLysGlnProAsnLeuGluGluileSerLysLeuLysFroAspLeuile 124 IleAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLyslleAlaProThr 144 64 45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValLeu GTTCAGGACGACGACGTTTACACTCGATAAAACGCCACAAGGGATTGTGGTGCTG 900 101 60 105 16 US-10-724-972A-6352 (1-335) x ACA32000 (1-900) Gaps: Score:
Percent Similarity:
Best Local Similarity:
Query Match: 20 85 125 g 8 ઠે 셤 ઠે g ઠે 셤

(ELIT-) ELITRA PHARM INC

27-NOV-2000; 22-DEC-2000; 16-FEB-2001;

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310 ATTGCCGACAGTCGCCATGCGGGATTTACACTGCCTTGCAGCAAATCGCGCCGGTA 369
                                                                                                                                                                          205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
                                                                                                                                                                                                                               225 GlnieuglyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu 244
                                                                                                                                                                                                                                                        ...----AACGTTCCCGCTGCGATG 633
                                                                                                                                                                                                                                                                                   245 LysGlyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg 263
                                                                                                                                                                                                                                                                                                                                    264 MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys 283
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490 ATGGCGCAGTCCAGCCAG-----CTTCCCACAGGACACGCGTGGCCTTTGGCACA
                        145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrlle
                                          SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys
                                                                                                                            IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal
                                                                                                                                                                                                544 TCACGCGAACAGCTATTCAACCTGCATACCCAGGAGACCTGGACCGGCAGCGTGCTGGCT
                                                                                                                                                                                                                                                                                                         634 GCGGGCGTCCATGCCGTCCATCGGCCTGGAGCAACTGCTGGCGGTCAATCCTGG
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745 GATCCGCTAGCTAGTTAACCGCCGCGCAGAGCAGCAGCTTCAGTCGACAGT
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26-MAY-2000;
23-OCT-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonala typhi, Klebsiela pneumoniae, coli, Staphylococcus aureus, Salmonala their provention is also useful for the identification of potential new targets for antibiotic consecul facelopment. The antisense nucleic acids can also be used to identify antibodies capable of binding to the expressed proteins, and to obtain the compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous colorations and the protein are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent coloration form part of the printed specification, but was obtained in the content of the coloration and the coloration in a coloration of the coloration and coloration in the coloration of the coloration and coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the coloration in the colorati
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Carr
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Trawick JD,
                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 909 BP; 200 A; 262 C; 261 G; 186 T; 0 U; 0 Other;
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                                                                                                                                                                                   Claim 27; SEQ ID NO 6372; 511pp; English.
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  Zyskind JW,
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Best Local Similarity:
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    Haselbeck R,
Yamamoto RT,
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 224
                                                                                                                                                                                       AspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg
AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
                                                                                                                                         MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys
                                                                                                                                                              CTGCTGGTTGCCCACTATCGC-----GAAGAGAGCATTGTTAAACGCTGGCAACAA
                                                                                                                                                                                                           GATCCGCTCTGGCAGATGTTAACCGCGCGCAGAAGCAGGTTGCTTCGGTCGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind JW;
Xu HH;
                     550 TCACGCGAACAGCAATTCAACCTGCATACTCAGGAGACCTGGACCGGCAGCGTGCTGGCC
                                              225 GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu
                                                                                           245 LysGlyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg
                                                                                                            AspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuVal
                                                                      -----AACGITCCCGCTGCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or E
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense, ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
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Yamamoto R,
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                                                                      610 TCTCTGGGGCTG-------
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362851.
06-MAR-2002; 2002US-0362851.
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Trawick JD,
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"I'm a vector comptriants a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host call contenting the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of the fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation; (8) required for proliferation, or that inhibits proliferation or the biological pathway in which a proliferation-required gene or its gene product lites or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism. The antisense nucleic acids are useful for which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the code or (13) identifying the target of a compound that inhibits the code or cellular proliferation in cells other than S. aureus, S. typhimurium, C. for cellular proliferation in cells other than S. aureus, S. typhimurium, C. prokaryotic essential genes. Note: The sequence data for this patent did for proliferation in the printed specification, but was obtained in cellectuals.
      comprising a promoter
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BP; 200 A; 262 C; 261 G; 186 T; 0 U; 0 Other;

909 100 62 104 16 Length: Matches: Conservative: Mismatches: Indels: 5.01e-35 460.00 57.45% 35.46% 27.22% Percent Similarity: Best Local Similarity: Query Match:

(1-335) x ACA32751 (1-909) US-10-724-972A-6352

ValGlyThrargLysGlnProAsnLeuGluGlulleSerLysLeuLysProAspLeulle 124 76 GTTCAGGACGACGAGTTTACACTCGAAAAACGCCACAACGGATTGTGGTGCTG 135 AspAsnLysLysAsnArgilelleLysProLeuArgAspLysIleGlyLysTyrThrSer 104 lleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThr 144 11eGluleuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile 164 SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184 ATGGCGCAGCCAGCCAGCCAG-----CTTCCCAAAGGACACGCGTGGCCTTTGGCACA 549 64 84 45 IleLy8HisGluGlvGlyThrThrLysValProLy8HisProLysArgValValValLeu 11eGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 65 136 85 196 105 256 125 316 145 376 165 196 ઠે g ઠે a ò g ઠે g ઠે g 8 કે ò 셤 ਨੇ

The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIMR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIMR nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAS46232-AAS46278 represent

Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound.

2001-602769/68.

WPI; 2001-602769/ P-PSDB; AAU29336.

Disclosure; Page 178-184; 526pp; English.

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810
                                                                                                                                               mar regulated polypeptide; NIMR; microbial infection; antibacterial; ds.
          :::
TCACGCAAACAGCAATTCAACCTGCATACTCAGGAGCTGGACCGGGAGCGTGCTGGCC
205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
                                           ---AACGTTCCCGCTGCGATG
                                                                    MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys
                            GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu
                                                         245 LysglyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg
                                                                                                                   284 AspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsplleLeuAspArg
                                                                                                                            DNA encoding novel mar regulated protein (NIMR) #7.
                                                                                                                                                                                                                    5238/c
AAS46238 standard; DNA; 10244 BP.
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ACA45366 standard; DNA; 891

(first entry)

19-JUN-2003 ACA45366;

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RESULT 28
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                                                                                                                                                                                                                              GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp
                      Sequence 10244 BP; 2347 A; 2737 C; 2791 G; 2369 T; 0 U; 0 Other;
Escherichia coli NIMR coding sequences of the invention
                                                             10244
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                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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The invention relates to an isolated nuclear act completes any and the facts antisense sequences given in the specification where expression of the fall antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concoling a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contisense nucleic acid; (7) identifying a compound that influences the activity of proliferation or that has an activity against a biological pathway contisensed for proliferation, (7) identifying a compound that influences the activity of required for proliferation or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound accompound and the capable of the strains is present in a culture or collection of compound activity; (11) a culture comprising strains in which the gene contist is overexpressed or underexpressed; (12) determining the extent of which each of the strains is present in a culture or collection of the proliferation of an organism. The antisense nucleic acids required for identifying proteins or screening for homologous nucleic acids required contains and proverse and identifying proteins or for screening candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, R. pneumoniae or P. aeruginosa. The present sequence is one of the rarget prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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Forsyth RA,
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Yamamoto R,
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                                                                                                                  Prokaryotic essential gene #27023
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362851.
06-WAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC
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Trawick JD,
                                                                                                                                                                                                                          Pseudomonas syringae.
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                                                                                                                                                                                     drug design; gene.
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155 AsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGluGly 174 388 CAGGGCAGCCTGAAATCTGCCGGGCTGATCGGCATGGCGCTGGGCAAAGGCCCCGGAGATG 447 17 LeuPheValLeulleAlaThrAlaAlaCysGlyAsnAsnSerSerAsnSerSerLys 36 55 ProLysHisProLysArgValValLeuGluTyrSerPheValAspAlaLeuValAla 74 LysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThrMet 194 508 GACAGCAAC-----GTGCTGTTCGGCGTTGCCCGTGAAGACAGTTTCTCGGTCCACGGC 561 215 SerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAsp 234 LeuAspyalLysProvalGlyIleAlaAspAspAsnLysLysAsnArgIleIleLysPro 94 ValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAspLeu 305 GluSerSerLysAspGlyValGluileLysHisGluGluGlyThrThrLysVal-----LeuArgAspLyslleGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeuGlu GluileSerLysLeuLysProAspLeuileIleAlaAspAsnAsnArgHisLysGlyIle TyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysSerPheAspGlyAspTyr 195 AspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisPro 235 AspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr---254 ------GluThrLeuSerGlnValAsnProGluArgMetPhelle MetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu---GluLysAspPro ctgtggcaggtgctcggcgctgtaggtaataaacaggtggccgaagtcgacgggaatagc 891 110 60 104 48 Length:
Matches:
Conservative:
Mismatches: US-10-724-972A-6352 (1-335) x ACA45366 (1-891) Gaps: 1.86e-34 454.00 52.80% 34.16% 26.86% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: 37 13 75 148 115 268 40 88 95 208 135 175 634 . 982 601 267 694 No. ò 셤 ठे g ò g δ a ò 쉽 ઠે 셤 ò g ઠે g 요 <u>ድ</u> ઠે ò g 8 8 8 g ò g

Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen, pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis; gene; ds. TrpAlaArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGluLeu Pathogen specific antigen related staphylococcal DNA SEQ ID No 318 Antibacterial; virucide; fungicide; BP. ABT15032 standard; DNA; 990 (first entry) 326 SerLys 327 867 CTCAAG 06-MAR-2003 306 802 862 ABT15032; ABT150 ò

Staphylococcus sp. WO200259148-A2

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01-AUG-2002

21-JAN-2002; 2002WO-EP000546.

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154 387

26-JAN-2001; 2001AT-00000130.

(CIST-) CISTEM BIOTECHNOLOGIES GMBH.

Zauner W; Hafner M; C, Henics T, , Weichhart T, U, Klade C Dryla A, Ahsen U, Etz H, Meinke A, Nagy E, Von Minh DB, Vytvytska O, Tempelmaier B;

WPI; 2003-075410/07.

Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody

Example 7; Page 210; 252pp; English.

The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma consisted in a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the immunity. The hyperimmune serum-reactive antigens comprising any of the consistent hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The complex of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis. The autibody preparations may also correct include cancer, autoimmune diseases or infections may also treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This method for identifying and producing pathogen specific antigens of the invention.

Sequence 990 BP; 398 A; 141 C; 179 G; 272

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This sequence represents Staphylococcus aureus cbrA DNA. The cbrA protein c is predicted to have a molecular weight of about 36.8 kD and, along with c berB (AAY42332) and cbrC (AX42333), is thought to be involved in iron c regulation, based on amino acid sequence homology with known iron c regulation, based on amino acid sequence homology with known iron repulator proteins. S. aureus is a ubiquitous pathogen which causes infections in burns, cellulitis, eyelid infections, food poisoning, joint infections, neonatal conjunctivitis, osteomyelitis, skin infections, connections, neonatal conjunctivitis, osteomyelitis, skin infections, such infections, scalded skin syndrome and toxic shock syndrome. S. aureus is increasingly becoming resistant to known antibiotics, with many strains generally being multiply drug resistant. Methicillin-resistant S. aureus (MRSA) poses serious infection control problems, with many strains being multiply drug resistant.

CC methicillin-resistant S. aureus (MRSA) poses serious infection control problems, with the exception of the vancomycin-type glycopeptide antibiotics with the exception of the vancomycin-type glycopeptide contable used as antibiotics and it may be used as a vaccine to prevent or attenuate an infection caused by a member of the could be used as antibiotics and it may be used as a vaccine to staphylococcus genus. The protein, or antibodies against it can be used in immunoassays to detect Staphylococcus in a biological sample.

CC detect Staphylococcus mucleic acid sequences may also be used to detect Staphylococcus in a biological sample.
925 TATAAATCTTCATTAAAACTTATTGACGATTTATATGAA-----AAGTTAAATATGAA 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus genes and polypeptides, vectors and methods of
                                                                                                                                                                                                                                                                                                             detection; diagnosis; screening; antibiotic; resistance;
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P-PSDB; AAY42331.
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312 LeuIleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys 331
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          New isolated Staphylococcus nucleic acid molecules, used to develop products for the diagnosis, prevention and treatment of Staphylococcal infections.
                                                                                                                                   infection; therapy; diagnosis; vaccine; antibiotic;
                                                                                                                    Staphylococcus aureus iron regulation gene cbrA.
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985 AAACAATCAAAA 996
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P-PSDB; AAY31824.
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This is the nucleotide sequence of Staphylococcus aureus strain ISP3
(ATCC 202108) genomic DNA including the novel cbrA gene that codes for a 310-amino acid protein (see AAY1824) of predicted mol.wt. 36.8 kDa. The sequence was obtained from overlapping clones BTACA44 and BTAGU54, which span a single operon containing the cbrA, cbrB and cbrC genes (see AAY1889-91). CbrA shows sequence homology to known genes involved in iron regulation. The invention provides 11 novel genes (see AAX1988-92) of S. aureus and the polypeptides they encode (see AAX18181-27). Also provided are vectors, host cells, antibodies and hybridomas. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity, and to diagnostic methods for detecting Staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. Antagonists of cbrA may be useful as antibiotics to treat infections of S. aureus and other Staphylococcus spp. Also provided are novel vaccines for the prevention or attenuation of infection by Staphylococcus. The isolated nucleic acid molecule is also production of cbrA protein

Claim 1; Page 24; 102pp; English.

Sequence 999 BP; 402 A; 142 C; 180 G; 275 T; 0 U; 0 Other;

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The invention describes a new isolated nucleic acid molecule comprising: a sequence that is 95% identical to a fully defined sequence having 586-226 bp, or its complement; or a sequence encoding a polypeptide having a fully defined sequence comprising 136-691 amino acids, or its complement. The gene is Staphylococcus aureus gene. The nucleic acid is useful for preparing a vaccine against infection caused by Staphylococcus aureus. The methods are useful for preventing or attenuating an infection caused by a Staphylococcus, detecting Staphylococcus nucleic acids in a biological sample obtained from an animal, and detecting Staphylococcus antibodies in a biological sample obtained from an animal. This sequence
               New staphylococcus aureus gene, useful for preparing a vaccine against infection caused by Staphylococcus aureus.
LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys
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Mismatches:
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/*tag= a
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                                                                                                                                                                                                                   Staphylococcus aureus cbtrA DNA
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P-PSDB; ADF43556.
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18-MAR-1999;
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01-APR-1998;
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                                                                                                                                                                                          12-FEB-2004
                                                                                                                                        ADF43555
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        312
                                                           332
                                                                                                             RESULT 32
                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                              ADF43555
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GGGAATTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 132 133 GCAATGGGTACAGAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGT 192 252 107 373 AAAGTTAGAAATGAAAAAGTTTACGATCAATTATCTAAAATCGCACCAACAGTT----- 426 128 AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu 147 480 240 690 LeulysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGly 27 AsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis 47 GluGluGlyThrThrLysValProLysHisProLysArgValValLeuGluTyrSer 67 148 LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla 167 168 LeuglyLyscluGluGluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGlu 187 188 TyrLysLysClulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys 207 588 220 648 87 241 SeriyaTyrLeuLysGly-----ProTyrLeuGlnMetAsnThr---GluThrLeuSer 257 811 TTAGTTAAAAAGACTGAAAGGGAATGGACTTCAAGTAAAGAGTGGAAAAATTTAGACGCA 870 VallysAsnGlnArgVal---AspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysBLysBspSerLys 331 ||||||| :::::: |TATAAATCTTCATTAAAACTTATTGACGATTTATATGAA-----AAGTTAAATATTGAA 984 193 GCCACTGACGTCGCTGTATCTTTAGGTGTTAAACCTGTAGGTGCTGTAGAATCATGGACA PheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLys LysAsnArgllelleLysProLeuArgAspLyslleGlyLysTyrThrSerValGlyThr GlnValAsnProGluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSer SerGlyLeuLeuAlaHisProSerAsn-------SerTyrValGly GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 691 CANANACAAGTTGATAATGGTAAAGATATTATCCAACTTACATCTAAAAGGAAAAGCATTCCA 34 Indels: Gaps: US-10-724-972A-6352 (1-335) x ADF43555 (1-999) 23.96**%** 10 æ 28 69 73 48 88 253 541 208 589 221 258 278 293 931 Query Match: ò 셤 ò g ઠ a 요 ò 요 ò 셤 õ ઠે a ઠે 6 ይ g ò g ઠે 유 중 음 g 8 Op ठ Q 8 8 8 8 ò

Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful fproducing antibodies effective against Staphylococci infection. Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor; antibacterial; vaccine; gene; ds. Staphylococcal surface-exposed immunogenic polypeptide DNA Location/Qualifiers complement (998. .1990) (DSQU-) D-SQUARED BIOTECHNOLOGIES INC. Claim 4; Page 51-52; 62pp; English. BP. /product= "SEIP" 531/c ACC48531 standard; DNA; 2940 17-JUN-2002; 2002WO-US019224. 17-JUN-2001; 2001US-0298975P (first entry) LysAspAsnLys 335 |||| :::||| 985 AAACAATCAAAA 996 Staphylococcus aureus. WPI; 2003-300870/29. P-PSDB; ABR41864. WO2003020875-A2 11-AUG-2003 13-MAR-2003. ACC48531; 332 Scott DL; ACC48531, 10 ACC48531, 11 ACC48531, 12 ACC48531, 12 ACC48531, 12 ACC48531, 13 ACC48

The present sequence is that of DNA encoding novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP) D2 SA02. To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SBIP antisera. DNA was isolated from clones expressing SEIPs, and functional domains. The SEIP encoded by the present DNA sequence has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococcal antibodies useful in staphylococcal infection. They can also be used to develop diagnostic

for

512 G; 959 T; 0 U; 0 Other; Sequence 2940 BP; 955 A; 514 C;

2940 113 65 132 34 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 4.57e-29 405.00 51.74% 32.85% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores:

US-10-724-972A-6352 (1-335) x ACC48531 (1-2940)

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27 8

(first entry)

16-MAR-1999

AAV74549

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1246 TIPATGAACGCTGATCATATTTTTGTAGTAAAATCAGAATCCCAAATGCGAAAGATGCTGCA 1187
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                                                       1924 GGGAATTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 1865
                                                                                                                                                           CAAAAACCGAAATTCGAATACATAAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA 1685
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1978 ATTAAAATGCTT----GTTGTTACGCTTGCTTTCCTACTTGTT----TTAGCAGGATGTAGT 1925
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                                                                                                                                                                                                 LysAsnArgileileLysProLeuArgAspLysileGlyLysTyrThrSerValGlyThr 107
                                                                                   48 GluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSer 67
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                                                                                                              .864 GCAATGGGTACAACTGAAATTAAAGGGAAACCAAAGCGTGTTGTTACGCTATATCAAGGT
                                                                                                                                           68 PhevalaspalaLeuvalalaLeuAspvalLysProvalGlylleAlaAspAspAsnLys
                           28 AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis
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1348 GAAATCTTAAATGATTTAGGATTCAAACGT----
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AAV74549 standard; DNA; 3775 BP.

AAV74549 ID AAV7

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable cof the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access commercial by a sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are composition against Saureus infection. The be used in a vaccine composition against Saureus infection of collypeptides can also be used in a kit for the immunodetection of Saureus in a sample. Saureus is implicated in numerous human diseases, containing cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used (and their fragments) are useful as primers or probes for isolating readable medium
                                                                                                                                                                                                                                                                              /*tag= a //note= "these bases represent a line of missing text in /note= "thesequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                             of missing text in
                                                                                                            Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide(s) and proteins derived from Staphylococcus aureus -stored on computer readable medium and used in the production of anti-S.aureus vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                          /note= "these bases represent a line of missing text the sequence listing in the specification. They are included to maintain the nucleotide numbering given the specification for this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fannon MR,
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65
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1021-1023; 3271pp; English.
                                                                               Staphylococcus aureus contig SEQ ID #238.
                                                                                                                                                                                                                                      Location/Qualifiers
1561. .1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
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51.74%
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                                                                                                                                                                       toxic shock syndrome; ds
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                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                      misc feature
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RESULT

BP. ACA21545 standard; DNA; 972

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ACA21545;

Prokaryotic essential

19-JUN-2003 (first entry)

gene #3202

ds; prokaryotic essential gene; cell proliferation; drug design; gene. Antisense;

Bacillus anthracis

WO200277183-A2.

03-OCT-2002

21-MAR-2002; 2002WO-US009107

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-00948993. 08-FEB-2002; 2002US-0072851. 06-MAR-2002; 2002US-0362699P.

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ሯ g ઠે 셤 ઠે 요

(ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Zamudio C, Malone C, Trawick JD, Carr GJ, o,r Wang Wall

2003-029926/02 P-PSDB; ABU17675

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 9415; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cacid; (2) a host cell containing the vector; (3) an isolated cacid; (2) a host cell containing the vector; (3) an isolated catid; (2) a host cell containing the vector; (3) an isolated catid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the cativity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway capable of specifically binding to proliferation, or that inhibits cellular proliferation; (8) cerquired for proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibicit; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which the trains or (13) identifying the target of a compound that inhibits the conformal configuration of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound cacids are useful for cellular proliferation to isolate candidate molecic acids required for required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target

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167 522 582 630 220 240 ||||||| ::: :: :: TATAAATCTTCATTAATATGAGTTTATATGAA-----AAGTTAAATATTGAA 1026 174 88 LysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrServalGlyThr 107 295 CAAAAACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA 354 108 ArglysGlnProAsnLeuGluGlulleSerLysLeuLysProAspLeulleIleAlaAsp 127 GAACCTGCACTAAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCA 414 128 AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu 147 468 reuglytysgiuglugiuglybysbyrgteugludluHisAspLystysIlegluglu 187 9 207 732 SerlysTyrLeuLysGly-----ProTyrLeuGlnMetAsnThr---GluThrLeuSer 257 27 47 67 258 GlnValAsnProGluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSer 277 278 Leu------LysGluLeuGluLysAspProValTrpLysLysLysLeuAsnAla 292 853 TTAGTTAAAAGACTGAAAGCGAATGGACTTCAAGTAAAGAGTGGAAAAATTTAGACGCA 912 293 ValiysAsnGlnArgVal---AspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys 331 LeuLys11eLeuSerVal11eGlyLeuLeuPheValLeuI1eAlaThrAlaAlaCysGly AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis 115 GGGAATTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 48 GluGluGlyThrThrLysValProLysHisProLysArgValValLeuGluTyrSer 68 PheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLys 235 GCCACTGACGTCGCTGTATCTTTAGGTGTTAAAACCTGTAGGTGCTGTAGAATCATGGACA 148 LysserPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla ---TCTACTGATACAGTTTTCAAATTCAAA---GATACAACTAAGTTAATGGGGAAAGCT 415 AAAGTTAGAAAATGAAAAAGTTTACGATCAATTATCTAAAATCGCACCAACAGTT-----TyrLysLysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys -----SerTyrValGly :::: :::::: GCTTCAGTTGTTAACTTCCGTGGTGATCATACAAGAATTTAATGCTGGTGGATAHGCTGĠT GlnPheLeuSerGlnLeuGlyPheLygGluAlaLeuSerAspAspValThrLygGlyLeu 132 34 12 SerGlyLeuLeuAlaHisProSerAsn------Mismatches: Indels: Gaps: (1-3775)US-10-724-972A-6352 (1-335) x AAV74549 32.85% 23.96% Best Local Similarity: 28 469 355 168 523 188 583 208 531 241 312 373 221 913 Query Match:

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LeuleuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLys 229
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                                                                                                                                                                                                                                                                                                                          GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp 84
prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 ATCTTAACT-----GACAATTCTTTAGCTTTACAAAAAAAAATTAGGT-----
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                                                                                                                                                                                      LysilereuSerValileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsn
                                                                                                                                                                                                       194 MetAspiysAsnGlnLysValLeuProAlaValAlaAlaLysSer----
                                                       U; 0 Other;
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1116
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122
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The invention describes a method of monitoring differential expression of the genes in cher Bacillus cells comprising hybridising labelled nucleic acid probes other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus (GCT), examining the array, and determining centaive gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of centain a first Bacillus cells The method is useful for monitoring one amore second Bacillus cells. The method is useful for monitoring in one or more second Bacillus cells. The method is useful for monitoring consistent in a first Bacillus cells and the function of unknown open reading frames and genes identifying possible functions of subschilty. Monitoring changes in expression of genes may be used to provide a representation of the way in white Bacillus cells adapt to changes in culture conditions.

CC in which Bacillus cells adapt to changes in culture conditions.

CC gene or one open reading frame, since sequence information is available.

CC gene or one open reading frame, since sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form to part of the printed specification, but was obtained in electronic format controlly from WIPO at ftp. wipo.int/pub/published_pcl_equences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                       308
                                                                                                         AsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLys
                                   LysieuAsnAlaValiysAsnGlnArgValAspIleieuAspArgAspLeuTrpAlaArg
                                                                                                                                             309 SerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeu 325
                                                                                                                                                                    tag; GST;
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                                   799 GATGAAGATAACATTTTTGACACGCAACTAAAA-
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                                                                                                                                                                                                                                                                                                                                                                           Bacillus licheniformis genomic sequence
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27-MAR-2001; 2001US-0279526P.
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                                                                                                                                                                                                                                                                standard; DNA; 944
                                                                                                                                                                                                                                                                                                                                                                                                                             altered culture condition;
physiological provocation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus licheniformis.
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Sequence 944 BP; 332 A; 197 C; 207 G; 208 T; 0 U; 0 Other;		Pred. No.: 2.6e-27 Length: 944 Score: 380.50 Matches: 109 Percent Similarity: 52.92% Conservative: 63 Best Local Similarity: 33.54% Mismatches: 128 Ouery Match: 23.51% Table 128		8 LeuLyglleLeuSerVallleGlyLeuLeuPheValLeulleAlaThrAlaAlaCyg 26		27 GlyabnabnSerSerabnSerSerlybGluSerSerlybabgpGlyvalGlulle 45		AAACACAACAGGACACAACAGATGTA	bo lyrberPheValAspAlaLeuValAlaLeuAspValLysProValGlylleAla 83 :::::	AspAspAsnLysLysAsnArgIleIleLysProLeuArgAspLysIleGlyLysTrrThr		104 SerValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeu 123 			144 ThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAsp 159	ACGATCGACATTGAGCTTGACCAGAAGAACTA	160 AlaPheLysThrlleSerLysAlaLeuGlyLysGluGluGluGlyGlygLysLysBrgLeuGlu 179 	3lulleThrMetABpLysABnGlnLys 19	57	ValLeuProAlaValAlaAlaLysSerGlyLeu			GOLITORICALONICACOLITORO CONTRACTOR CONTRACT		260 AsnProGluArgMetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeu 278		279 LysGluLeuGluLysAspProValTrpLysLeuAsnAlaValLysAsnGlnArgVal 298 :: ::::: :::	31
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food cuspidement. (II) and its binding partners are useful in medical imaging of supplement protein expression or biological activity. The colypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of muterions can be produce other types of data and products dependent on DNA and responsible for genetic disorders or other traits to assess biodiversity coding sequences AAS64497-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this coding sequences of the invention. Note: The sequence data for this celectronic format directly from WIPO at the enter of the coding accuence of the invention are sequenced to the coding accuences of the invention. Note: The sequence data for this celectronic format directly from WIPO at the coding accuences of the coding accuences of the coding accuences of the coding accuence data for this content with the printed specification, but was obtained in the printed specification, but was obtained in the printed of the coding accuences of the coding accuences of the coding accuences of the coding accuences of the coding accuences of the coding accuences of the coding accuence of the coding accuence of the coding accuence of the coding accuence of the coding accuence of the coding accuence of the coding accuence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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916 ATGGTGAAAGAAGTC 930
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23-AUG-2000; 2000US-00649167.
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P-PSDB; ABG07192.
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                                                                                         GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu 244
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                                                         165 SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184
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The invention relates to isolated polynucleotide (I) and polypeptide (II) captences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed conservative of (II) is useful in gene therapy techniques to restore normal carivity of (II) or to treat disease states involving of (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in conversions of diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and conversion of the produce other types of data and products dependent on DNA and aming an action sequences. Assettly the convent human diagnostic
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                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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23-AUG-2000; 2000US-00649167.
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P-PSDB; ABG08851.
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EP786519-A2

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97EP-00100117. 07-JAN-1997;

96US-0009861P. 05-JAN-1996;

SCI INC. (HUMA-) HUMAN GENOME

Ŗ, Rosen Ж, , Fannon 진, Dillon Barash SC, Choi GH, Kunsch CA,

WPI; 1997-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus -stored on computer readable medium and used in the production of anti-.aureus vaccines.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable cof the invention. The DNA sequences are recorded on a computer readable commedium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or CD-ROW. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CC be used in a vaccine composition against S.aureus innuncdetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteonyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences come computer computer computer.

U; 60 Other; 0 : G; 190 Sequence 668 BP; 216 A; 83 C; 119

668 71 15 36 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 4.96e-25 355.00 70.49% 58.20% 21.01% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

US-10-724-972A-6352 (1-335) x AAV74666 (1-668)

61 210 LeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLys 2 TTATTAGCACATCCAAACTATTCATATGTTGGACAATTTTTAAACGAACTAGGATTTAAAN ð 셤

230 GluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeu 셤 ò

GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhelleMetThrAsn 250

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181 289 241

270 LysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLys

LeuAsnAlaVallysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSer 309 290

Claim 1; Page 1239-1240; 3271pp; English. readable medium

------GluMetAlaLysGluLeuValGluLeuSerLys 327 317

GACGAAGCCGGTGAAGATGCGAAACTGGTTGCGGTTCCGCCACCAGCTGAGCAAAGAA

------AspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerGlu

849

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736 302 790

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285 ProvalTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsplleLeu-----

694 TCTATCCATGCAATTACGGTTACATCAACCACCCCTCTCTC

AAV74666 standard; DNA; 668

AAV74666;

(first entry) 16-MAR-1999

Staphylococcus aureus contig SEQ ID #355.

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

Staphylococcus aureus.

misc_feature

Location/Qualifiers 61. .120 /*tag= a /note= "these bases represent a line of missing text

in

309 124 | IlealaaspasnasnargHisLysGlyIleTyrLysAspLeuasnLysIlealaProThr 144 164 184 489 204 543 224 603 GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu 244 245 LysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMet 264 265 PheileMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAsp 284 AspAsnLysLysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSer ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile SerLysAlaLeuGlyLysGluGluGluGlyClysLysArgLeuGluGluHisAspLysLys GGCGAAATGGTGGTAAAAGCGAGAGATGCAGGCACGTCTGGAACAACATAAAGAGAGG 185 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer -----AACGTTCCCGCTGCGATG 634 GCGGGTGCGTCCTCGCCTCGTCCGCTGGTCCGCTTCATGTCCACGCGATGT 604 TCTCTGGGGCTG-----

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) concention relates to isolated polynucleotides, polymerase chain sequences. (I) is useful as hybridisation probes, polymerase chain concention (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed concention of useful in gene therapy techniques to restore normal cuseful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and (II) and (II) and (II) and (II) are useful for treating disorders of stress expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in companies for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences Aps644197-AAAS94564 represent novel human disapnostic coding sequences of the invention. Nove: The sequence data for this patent did not appear in the printed specification, but was obtained in companies of the invention. Nove: The sequence data for this content views. The sequences of the invention was pecification, but was obtained in the printed pecification, but was obtained in the printed pecification, but was obtained in the printed pecification, but was obtained in the printed pecification, but was obtained in the printed pecification, but was obtained in the printed pecification.
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TIGAAIGCAGIIAAAAAIAAICGCGIGGAIAIIGIIGACCGIGAIGIITGGGCAAGAICI 301
                                       310 ArgGlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                          forensic;
                                                                                                                                                                                                                                                                                                                                                                                                          Human, chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2799 BP; 619 A; 740 C; 776 G; 664 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                              encoding novel human diagnostic protein #13139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 13139; 103pp; English.
                                                                                                                                                                                                                                                   AAS77335 standard; cDNA; 2799 BP.
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23-AUG-2000; 2000US-00649167
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                                                                                                                           SerLys 331
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Alignment Scores:

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2032 GGCGAAATGGTGGGTAAAAGCGAGAGATGCAGGCACGTCTGGAACATAAAGATAAGAGG 2091
                                                                                                                                                                                                                                                                  105 ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 124
                                                                                                                                                                                                                                                                                                                     125 ilealaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysileAlaProThr 144
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                                                                                                                                                                                                                                            AspAsnLysLysAsnArgilelleLysProLeuArgAspLyslleGlyLysTyrThrSer 104
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                                                                                                                                                                                                                                                                                                                                                                                                                      145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile
                                                                                                                               45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValLeu
                                                                                                                                                                                       GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlylleAlaAsp
2799
69
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                 Matches:
Conservative:
Mismatches:
Indels:
                                                                                                    US-10-724-972A-6352 (1-335) x AAS77335 (1-2799)
     Length:
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Job time : 749 secs
                                                                            Gaps:
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    9.06e-24
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20.71%
                                  Percent Similarity:
Best Local Similarity:
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                                                                Query Match:
DB:
       No.:
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BJ347654
AZ532836
AZ532836
CL957361
BH132864
BH0065769
CCF109973
AX407955
CC573945
BJ71489
AX012454
AX549761
CC0113362
AZ549761
CR650378
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BW448137
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CR426562
CR731171
CR685229
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ALG66132
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2005, 19:55:21; Search time 3860 Seconds (without alignments)
3303.505 Million cell updates/sec
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US-10-724-972A-6352

Perfect score:

Scoring table: Sequence:

34239544 seqs, 19032134700 residues

Searched:

), Xgapext), Ygapext), Fgapext), Delext

BLOSUM62 Xgapop 10.0 , Xg Ygapop 10.0 , Yg Fgapop 6.0 , Fg Delop 6.0 , Dd

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Homo sapi AGENCOURT BJ714899

Mus muscu

OSIFCC000 ENTOP58TR Mus muscu AGENCOURT Shultzomi

AZ532836 AZ538305 CL957361 CH132864 AK029960 BQ065769

ENTDA85TF

GR Eb013 ENTFK51TF Tetraodon

AY407955 CO573945 BU714899 AK012454 CO113362 AZ549761 CK650378 AL854856 BW253010 BW254793

AL854856 BW253010 BW254793

BW222839

BW222839 BW235942

Mus muscu CR426562

Tetraodon Tetraodon

BJ706325

BW055754 BY00525 AY420059 CR426562 CR431171 CR6312171 BJ706122 BJ706122 BJ712865 BJ712865 BJ712865 BJ712865 BJ712865 BJ712865 BJ712865 BJ712865 BJ712865 BJ712865 BJ712865

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ALIGNMENTS

Command line parameters:
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-DBV_TIMEOUT=120 -WARN TIMEOUT=30 -THREAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

summaries

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

	Descripti	Ö
436	L694436	PR:
627	27	PR
287	F307287	HD
885	385	ESJ
049	L682049	PRJ
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106	CL958706 (Osj

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_est2:* gb_htc:* gb_est3:*

gb_est1:* gb_est2:*

EST: *

Database

9b_est4:* 9b_est5:* 9b_est6:* 9b_9ss1:* 9b_9ss2:*

SUMMARIES

Score

Result Š. U

Description	L694436 PRIO	CL674627 PRI0112c_	CF307287 HDA106-	BE432885 EST399330	CL682049 PRI0132d	AL151412 Anopheles	CL958706 OSIFCC001	CL665859 PRI014d G	CL666398 PRI01525
ID	립	CL674627	CF307287	BE432885	CL682049	CNS01MUR	CL958706	CL665859	CL666398
90	١٥	σ	7	~	6	6	σ	σ	0
Query Match Length DB	977	801	625	531	160	996	2019	810	881
Query Match	24.4	24.3	21.8	12.4	9.0	7.6	7.5	7.2	7.2

152 126.5 122 122

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/organism="Pristionchus pacificus" /mol_type="genomic DNA"

us-10-724-972a-6352.rst

version 5.1.6 - 2005 Compugen Ltd.

GenCore Copyright (c) 1993

OM protein - nucleic search, using frame_plus_p2n model

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November

Run on:

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IlealaaspasnasnarghisLysGlyIleTyrLysAspLeuAsnLysIlealaProThr 144
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                                                                                                                              1 (bases 1 to 801)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. Appable: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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                                                                                                   Bukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida.
Neodiplogasteridae, Pristionchus.
                                                                                                                                                                                                                     Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Eas: 00497071601439
Email: ralf. sommerætuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
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/mol_type="genomic DNA"
/strain="California"
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               survey sequence.
CL674627
CL674627.1 GI:50177972
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                                                                                                                                                                                                                                                                                                                                         959
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var. California"
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                                                         /note="Vector: pEpifos-5 Fosmid vector"
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531 bp mRNA linear EST 18-MAY-2001
EST399330 tomato breaker fruit, TIGR Lycoperation esculentum cDNA
clone cLEG10K14, mRNA sequence.
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Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
                                                                                                                                                                                                                     GCCGAAATGGTGGGTAAAAAGCGAGAGATGCAGGCACGTCTGGAACAACAACATAAAGAGAGG 200
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                                                                                                                                            GITCAGGAACAGACAGTITACACTCGAAAAACGCCACAACGGATIGIGGTGCTG
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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SM Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

E 1 (bases 1 to 625)

S Kim,J.S., Jun,K.M., Cheong, P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6155
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                                           ATGGCGCAGTGGGCCAGCCAG-----CTTCCCAAAGGGACACGCGTGGCCTTTGGCACA 552
                                                                                                                                                                                                                                                                            702
                                                                                       205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
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                                                                                                                                                                                                                                        245 LysGlyProTyrLeu---GlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg 263
                                                                                                                                                                                                                                                                                                                MetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys 283
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-----AACGTTCCCGCTGCGATG
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                                                                                                                                                                                                                                                                                                                                                                                      AspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgVal 298
                                                                                                                                                                                                                                                                                                                                                                                                           Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
    Location/Qualifiers
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                                                                                                                                                                              P. pacificus
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Location/Qualifiers
1. .760
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the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
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Neodiplogasteridae; Pristionchus.

I (Dases 1 to 760)

S Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus

L Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601371
Fax: 0049707160148
Email: raif: sommer@tuebingen.mpg.de
This library was generated at Caltech, Passadena, USA and end sequenced at Vancouver, Canada.
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Class: fosmid ends.
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CLM58706 11near GSS 21-SEP-2004 OBJECC001947 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. CL958706
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Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
I (basea; 1 to 2019)
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
Manalysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
                   ----GlylleTyrLysAspLeuAsnLysIleAlaProThrlleGluLeuLy 148
                                           441 GGATTCCGCGCTGGCGCTGTACGATCAGCTTTCCGCCATTGCGCCGACGCTTATCATCA 500
                                                                                                 148 sSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLe 168
                                                                                                                                                                                uGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTy 188
                                                                                                                                                                                                        GCATTCCGCCAACCTTTKGACC----ACGGAATCGGCACAGGGCAAGCTGCTGCACCA 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGln--ValAsn
                                                                                                                                                                                                                                                                     rLysLysGluIleThrMetAspLys-----AsnGlnLysValLeuProAlaValAl
                                                                                                                                                                                                                                                                                                                                                   aAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGl
                                                                                                                                         501 CTACKACGACAAGAGCTGGCAGGTGCTGCTGACCCAGCTGGGCGAGATCACC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
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Class: exon-trapped.
Location/Qualifiers
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Fax: 86-10-80488676
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                                                                                                                       CNS01MUR 966 bp DNA linear GSS 14-JUN-2001
Anopheles gambiae GSS T7 end of clone 22J04 of NotreDamel library
from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
2 (bases 1 to 96)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 CGACCACGCCGAACAACCGCGTGGCGNATGGACAGGGTTTCCTGCGCCA----- 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 -GTGGGGCGATATGGCGAA----CARCGCAAGGTTGCCCGGCTGTATATCGGCGAGCC 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GlulleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValVal 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-PEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                  Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
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67
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116
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Mismatches:
Indels:
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/organism="Anopheles gambiae"
/organism="Pes"
/strain="PesT"
/db_xref="taxon:7165"
/clone="2200"
/clone lib="NotreDame1"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 sileglyLysTyrThrSerValGlyThrArgLys-
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43.21%
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  298
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298 Val
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CNS01MUR
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CL665859 810 bp DNA linear GSS 09-JUL-2004 PRI014d G07 - PRI014d B21 (810) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic genomic
-AATGAGTTGCTGCGTCTCGCAATT 1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsn 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 AsnThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsnLysAla 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:54126"
/clone_lb="mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                       Stindages 1.0 Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppaDB: an AcedB database for the nematode satellite organism Pristinchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------AACGTTCCCGCTGCGATGCCGGTGCGTCCATGCCGTCCATC
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 CATACTCAGGAGACCTGGACCGGCAGCGTGCTGCTCTCTGGGGCTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
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1 (bases 1 to 810)
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/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                                                                 1954 GCTGAGGCACAGGAAAAGAATAAG 1977
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122.00
48.25$
25.44$
7.22$
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Class: fosmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1780 GCATTA-----GATGTTGAGAAGGTTGAAGCATGTAAGCTGAAGTCAAAATTTAAGGAA 1833
                                                                                                                                                                                                                                                    GCACAACAGAAACAAAGCATATTAGAAGTAGAGGCTAACAATCTCAAGATGGAATTGGGT 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 ArgilellelysProLeuArgAspLyslleGlyLysTyrThrSerValGlyThrArgLys 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 GlnProAsnLeuGluGluIleSerLysLeuLysProAspLeulleIleAlaAspAsnAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 AsnAlaVal------LysAsnGlnArgValAspIleLeudspArgAspLeuTrpAla 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 ArgSerArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLys 327
                                                                                                                                                                                                                                                                                                    ---ValAsp 70
                                                                                                                                                                                                                                                                                                                                                                          AlaLeuValAlaLeuAgpValLygProValGlyIle---AlaAspAspLysLygAsn 89
                                                                                                                                                                                                                          GluSerSerLysAspGlyValGluIleLysHisGluGluGlyThrThrLysValProLys 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1834 CTTGAAAAT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||||
|1576 GGGGACCTCAAGAGAAGATAGAGGAAATCCAGCTCAGCAAGGAAGCT-----GCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1690 CAAGTTTCTTTATCGCAACTACAAGCATCCTATAATGAACTTGATGCTAAAGCATTCTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaSerSerAsnGluProSerLeuLysGluLysAspProValTrpLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TATAAGGCTGAAAAGGATGAAGAGGCTGGGAAACTG
                                                      2019
74
55
114
85
                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 ThrileGlu-----LeuLysSerPheAsp----
                                                                                                                                                                                      (1-335) x CL958706 (1-2019)
                                                                                                                                                   Gaps:
                                                                       126.50
39.33
22.56
7.49
                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                      US-10-724-972A-6352
                                    Alignment Scores:
Pred. No.:
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA. This sequence as made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                 AY420057 4137 bp DNA linear GSS 12-DEC-2003
Homo sapiens HCM7097 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3016 TTGAGAGATAAGACAGTTCTCATTGAGAAGTCTCATGAAATGGAAAGAGCATTAAGCAGA 3075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACTAAAAGACCAGTTATCAGAGCAGACACAAAAGTATAGTGTCAGTGAAGAAGAAGTCA 2956
                    AjavalLysAsnGinArgvalAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysLysAsnArgileilelysProLeuArgAspLysileGlyLysTyrThrSerValGly 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnAsnSerSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis 47
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 4137)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, B., Ferritera, S., Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
                                              48 GluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheValAspAlaLeuValAlaLeuAspValLys---ProValGlyIleAlaAspAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kejariwal, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, J. Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ateriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                LeulleSerSerGluGluMetAlaLysGluLeuValGluLeu 325
                                                                                                                       570 ATTTTTGCTGCAGAGCGTATTGCCGCTGACACGGTAAAATC 529
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DN
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                          genomic survey sequence
                                                                                                                                                                                                                                                                                              AY420057.1 GI:39776014
                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .>4137
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Best Local Similarity:
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                      292
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KEYWORDS
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                                                                                                                                                                                             AY420057
LOCUS
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REFERENCE
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                                                                                                                                                                                           CL666398 101-2004 881 bp DNA linear GSS 09-JUL-2004 PRI0152b_E03 - PRI0152b.B21 (881) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
                                          295
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AlaValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 HisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeu 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 SerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsn 291
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of P. pacificus
                          233 SerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeu---GlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              831 CATACTCAGGAGACCTGGACCGGCAGCGTGCTGGCCTCTCTGGGGCTG--
                                                                          312 LeuIleSerSerGluGluMetAlaLysGluLeuValGluLeu 325
                                                                                                  296 ATTTTTGCTGCAGAGCGTATTGCCGCTGACACGGTAAAATC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:54126"
/clone_lib="mixed stage fosmid library
var. California"
/note="Vector: pSpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Max-Planck-İnstitute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              881
29
26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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Location/Qualifiers
                                                                                                                                                                                                                                                  survey sequence.
CL666398
CL666398.1 GI:50159122
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Pristionchus pacificus
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122.00
48.25%
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7.22%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 AspAlaPhe-------LysThrileSerLysAlaLeuGlyLysGluGluGlu 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 GlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThr 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaThrAlaAlaCysGlyAsnAsnSerSerAsnSerSerLysGluSerSerLysAsp
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/clone="dda27b21"
1111 Yata, Mishima, Shizuoka 4
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                        /mol_type="mRNA"
/strain="AX4"
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                                                                                                                                                                                                                                                                    3316 AAAGAGCAGCAGACAGTGACCAAACTGCATCAATTGTTGGAGAATCAAAAGAACTCTTCT 3375
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                                        107 ThrArglysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAla 126
                                                                                                       127 AspAsn-----AsnArgHis-------LysGlylleTyrLysAsp 137
                                                                                                                                                                        LeuAsnLysIleAlaProThrIle-----GluLeuLysSerPheAspGlyAspTyrAsn 155
                                                                                                                                                                                                                                       GluAsnileAspAlaPheLysThrileSerLysAlaLeuGlyLysGluGluGluGlyLys 175
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Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases I to 764)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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                                                             AATGTGAAAGAGAAGCTAGTAGAAGAAAATGCCAAAACAGACTTCTGAGATACTTGCAGTG
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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906 bp DNA linear GSS 14-NOV-2000
ENTFOGETF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Bukaryota; Entamoebidae; Entamoeba.
Bukaryota; Entamoebidae; Entamoeba.
B. Loftus, B., Van Aken, S. and Fraser, C.
Doftus, B., Van Aken, S. and Fraser, C.
Dottus, Brendan J. Loftus
Contect: Brendan J. Loftus
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The Institute for Genomic Research
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Tel: 301 838 9543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                          157 AsnileAspAlaPheLysThrileSerLysAlaLeuGlyLysGluGluGlyLysLys 176
                                                                                                                                                                                                                                                                                                                                                                                                       177 ArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLys 196
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Seg primer: M13-Forward
                                                                                                                     LeuLysProAspLeullelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeu 138
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                                                    139 AsnLysile-----AlaProThrIleGluLeuLysSerPheAspGlyAspTyrAsnGlu 156
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                                                                                                                                                                                                                                                              388 CAACAGTTATCAACAAGTACAACAAAGAAAAAAAAAAATTTGATCAAGAC-----
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/strain="HM1:IMSS"
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High quality sequence stop: 8
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/db xref="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Wetcor: pHOS1; Site=1: BET i; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                               Unpublished (2000)

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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
  ENTDA85TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                               Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 839)
Loftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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Seq primer: M13-Forward
Class: shorgun
High quality sequence start: 21
High quality sequence stop: 820.
Location/Qualifiers
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                           genomic, genomic survey sequence.
AZ532836
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/strain="HM1:IMSS"
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                                                                                                                     Entamoeba histolytica
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 IleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeu 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 AlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAla 231
                                                                                                                                                                                                                                                                                                                                                                                                                        42 GlyValGluIleLysHisGluGluGluGlyThrThrLysValProLysHisProLysArgVal 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGly
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CL957361 1782 bp DNA linear GSS 21-SEP-2004 OBIPCC000458 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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252 AsnThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThrAsnLysAla 271
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                                                                                                                    272 SerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsn
                                                           259 GAAGAAGAA-----AGACAAATAGAAGAAAAAGACAA-----ATAGAAGAAAAAG
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/mol_type="genomic DNA"
/db_xref="taxon:19946"
/db_xref="taxon:19946"
/dolo lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequen
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211 CAAACAAAAGAAATTATTACAACTTGAAGAAAAACAA-----
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Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80488559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
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1318 CTCCAGGAACTCCACGCCGAGAAATCAAAAGCATCCATTAGCAGTGAGAAGCAGATCTCC 1377
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859 GAAGGTGATCTAGCAAAAATGTCACAAGAAATTGCAGCTCGAGGCCCAGGTTAAGGAA 918
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                                                                                                                                           104 SerValGlyThrArgLysGlnProAsnLeu-------GluGluIleSerLysLeu 119
                                                                                                                                                                   703 AGCCTTCAGAAGGAACTTGAAGGCCAACTÁGCTCATCATGACCATGÁAÁTTGAGAÁGTGC 762
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                                      98
::: ||||||||| sas gaagacaagtccttttgcattgaacgaacgaatgcccagctagaagat
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919 CTTGAACAAGCATCTCGCAGCCTAGATGATTCATCAGCACAGATTATGAAGCTCCAAGAA
                                                                                        LysLys------AsnArgllelleLysProLeuArgAspLyslleGlyLysTyrThr
                                    SerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsn
                                                             GAGCTTCAGGAAGCAAGGGAAAAACTTGAG------GCACTTGAGGAAAAGAAT
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1483 GCTCGTGATGAGAG 1497
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/ Brania "HMI.IMDS."
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/ Clone_lib="Entamoeba histolytica Sheared DNA"
/ Clone_lib="Weator: 18051; Site_: 18 BS 1; Constructed at The
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Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects: In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)." 897 bp DNA linear GSS 07-AUG-2001 Entamoeba histolytica Sheared DNA Entamoeba histolytica Email: bjloftugetigr.org Clones are derived from the Entamoeba histolytica HM1:IMSS sheared MAN library Seq primer: M13-Reverse Class: shotgun |||| TCCAAGAAGGATAAAAAAAAATACCAGTGATGGAATGAAGGAGAATACGAAGAA----- 781 GATGGTATGATATCTTCAAGAAGTATATCAATC-----AAAAAGAAAAAGATA 703 ileLysProLeuArgAspLys1leGlyLysTyrThrSerValGlyThrArgLysGlnPro 111 -----ATACTTAAAAATATGAGGTAAAAGAAAA 751 ThrLysValProLysHisProLysArgValValValLeuGluTyrSerPheValAspAla 71 LeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLysAsnArgIle 91 Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HM1:IMSS sheared DNA library (2001) SerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHisGluGluGluGlyThr Unpublished (2001)
Context: Brendan J Loftus
Context: Brendan J Loftus
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 9308 897 68 57 1114 71 /organism="Entamoeba histolytica" /mol_type="genomic DNA" /strain="HM1:IMSS" Length: Matches: Conservative: Mismatches: Entamoeba histolytica Eukaryota, Entamoebidae, Entamoeba. 1 (bases 1 to 897) Indels: US-10-724-972A-6352 (1-335) x BH132864 (1-897) seguence. Gaps: High quality sequence start: 13 High quality sequence stop: 814 Location/Qualifiers genomic, genomic survey BH132864 92 ò

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/note="Organ: lymph; Vector: poTB7; Site_2: dadaptor:
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AGENCOURT 6875095 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5930336
5', mRNA Sequence.
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1062 GATTCTGTTGTGGAAGACTTA-----CATTTACAAAATAAATACCTTCAAGAAAAACTT 1115
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2109 row: o column: 09
High quality sequence stop: 670.
                                                                   224 SerGlnLeuGly-----PheLysGluAlaLeuSerAspAspValThrLysGlyLeu
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                                                                                                                                                                                                  241 SerLys------TyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSer
                                                                                                                                                                                                                                                                      1176 GAGTCAGATGATCACTGTCAAAAAGAACAAGAACTTCAGAAGGAAAATTTGAAGTTGTCA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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GESPHS FPIY"
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match=2139)"
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Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V., Bahulz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V., Padua,A.M., Gurske,M.L., Morin,D., Penn,S.G., Jovanovich,S.B., Plopper,C.G. and Buckpit.A.R.
Gene expression analysis in response to lung toxicants: I. Sequencing and microarray development
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Contact: Shultz MA biosciences, School of Veterinary Medicine University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA Tel: 530 752 4698
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                                                               CF109973 1005 bp mRNA linear EST 23-JUL-2003 Shultzomica03224 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone Contig2841 5', mRNA sequence.
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/dev_stage="adult"
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Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
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                                                                                                                                                                                                                             Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 AAAACAAGTTTTGATGAGAATGATAGTGAAGATTGGAAGATAAAGATTCAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/clone="Contig2841"
                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
                                                                                                                                      CF109973
CF109973.1 GI:33165360
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KEYWORDS
SOURCE
ORGANISM
                                                                                         DEFINITION
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COMMENT
                       RESULT 18
CF109973
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                                                                                                                                      ACCESSION
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                     0.0265
1117.50
37.97%
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Best Local Similarity: 18.96% Mismatches: 146 Query Match: 6.92% Indels: 103 DB: 9 Gaps: 11	US-10-724-972A-6352 (1-335) x AY407955 (1-5504) Qy 22 AlaThrAlaAlaCysGlyAsnAsnSerSerEserEysGluSerSerLysAsp 41		Qy 42 Gly-ValGluIleLysHisGluGluGlyThrThrLysValProLysHisPr 58	Oy 58 olygArgValValValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLy 78	Db 4257 AAAGACCAAGAACAGGCTTCAGCAGGAGCTGGATGTTGTTTTGGACAACCA 431 Qy 78 8ProValGly11eAlaAspAspAsnLysLysAsnArg11e11eLysProLeu 95		GGAGAAAAACATCTCTTCCAAATACGCGGATGAGGGACAGAGCTGAGGCAGAAGCCAG	Db 4437 GGAGAAACCAAAGGCCCTGTCCCTGGCTCGGCCCTTGAAGAGCCTTTGGAAGCCAA 4496		126	bb 4557 CAAGGATGAGGAAGAGCGTCCATGAGCAGAGAGTCCAAGCGGGCCCTGGAGAC 4616	Qy 137Ag 137	Db 4617 CCAGATGGAGGAGATGAAGACGCAGCTGGAAGACTGGAGGACGAGCTGCAAGCCACGGA 4676	Qy 137 pLeuAsnLysIleAlaProThrIleGluLeuLysSerPheAspGlyAspTyrAsnGluAs 157 : ::::::: ::::::::: :::::::::::	157 nIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGluGlyLysLysAr	Db 4737 TCTCCAAGCC	4770 GAGGAGGAACTGCAGAGTTCACGAGTATGAGACGGAACTGGAAGAGGGAAA	Oy 197 nGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSe 217	217 rTyrValGlyGlnPheLeuSerGlnLeuGlyPheLygGluAlaLeuSerAspAspValTh		237	4911 CAAGGGGAGGAAGCCATCAAGCAGCTACGCAAACTGCAGGCTCAGATGAAGGACTT	Oy 253 -ThrGluThrLeuSerGinValAsnProGluArgMetPhelleMetThrAsnLysAlaSe 272	272 rSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLysLeuAsnAl
Oy 94 ProLeuArgAspLysIleGlyLysTyrThrSerValGlyThrArgLysGlnProAsnLeu 113 Db 602TCTAAAAAAGGTAAAAAAGGCCAGAAATCAACTAAAAAAAGGGTGG 652	Qy 114 GluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnArg 130 Db 653 GAAGAGGATGAA		Db 686 GAACGTICGAGAGTAAACTCCTCAGGTGAAAGTGGTGAGTCTGATGAATTTTTGCAG 745 Qy 131HisLysGlylleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLys 148		Qy 149 SerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLys 166 :::	Qy 167 AlaLeuGlyLysGluGluGluGlyLysLysRygLeuGluGluHisAspLysLysIleGlu 186	Oy 187 GlufyrLysLysGluIleThrMetAspLysAsnGlnLys 199 :::	SULT 19	A1407955 LOCUS A1407955 S504 bp DNA linear GSS 15-DEC-2003 DEFINITION Homo sapiens MYH11 gene, VIRTUAL TRANSCRIPT, partial sequence,	ACCESSION 51407955 VERSION AY407955.1 GI:39763926	KEYWORDS GSS. SOURCE ORGANISM Homo sapiens (human)		REFERENCE 1 (bases 1 to 5504) AUTHORS Clark A G. Glanowski S. Nielson P. Thomas D. Keiariwal B.	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.	TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios JOURNAL Science 302 (5652), 1960-1963 (2003)	146.1302 2 (bases 1 to 5504) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwa	Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,	TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, HSA		FEATURES Location/Qualifiers Source 1. 5504	/mol/db/	gene <1>5504 /gene="MYH11"	/ IOCUB_tag="HLM3063"	Alignment Scores: 0.328 Length: 5504 Pred. No.: 0.328 Length: 5504 Score: 117.00 Matches: 73 Percent Similarity: 35.32% Conservative: 63

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BJ714899 BF01FFA CDNA Oryzias latipes CDNA clone MF01FFA033h02 5', mRNA sequence.
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/ Ab xref="taxon:10116"
/ Ab host="IMAGE:132914"
/ Ab host="IMAGE:132914"
/ Ab host="IMAGE:132914"
/ Ab host="DH10B TOAA"
/ Clone lib="NIH MGC_246"
/ Ab host="Gran: liver; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before animal. Tissues were snap-frozen and kept at concept animals. Tissues of purification (Tri-reagent method). CDNA was primed using oligo-dT primer:
5-pGACTAGTTCTAGATCGCAGCGCCCCC(T) 25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.7 kb. This a primary library (normalized library is NIH MGC 247) and was constructed by Open Biosystems. Note: this is a NIH MGC library"
                                                                                                                                                                                                                                                                                                                                       CO573945
AGENCOURT 28537271 NIH MGC 246 Rattus norvegicus cDNA clone
MMGE:7272914 5', mRNA sequence.
                                                                                                                                  Nature:

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Intomal Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0Ad7 Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical

College of Wisconsin

College of Wisconsin

College of Wisconsin

College of Wisconsin

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  292 aValLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGlyLe 312
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Conservative:
Mismatches:
Indels:
Gaps:

    .804
    organism="Rattus norvegicus"

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Rattus norvegicus
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CO573945.1 GI:50386574
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.

1 (bases 1 to 832)

Mobara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
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65
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67
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tal: Nata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                  /db_xref="taxon:8090"
/clone="MF01FFA033h02"
/sex="mixture of female and mc/tissue_type="whole embryo"
/dev stage="fry stage 40"
/clone_lib="MF01FFA cDNA"
                                                                                                                                                                                                                organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         x BJ714899 (1-832)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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/strain="Hd-rR"
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41.04%
24.25%
6.89%
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                 261
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 1545)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                       ||| ::||| ::|||
-------ATGAAGTCAACTGTGGAAGATGAGAAGCTTGCTGGCAAGATCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro
                                                                                                                                                                                              262 GluargMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu
LeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGly---LeuSer
                                                                                                                                                                                                                                                                                                                               701 AACCAG------ACTGCCGAAAGAGATGAGTACGAGCACCAACAGAAGGAGCTT
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full-length
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Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK012454 Innear Mus musculus 11 days embryo whole body cDNA, RIKEN enriched library, clone:2700059D02 product:similar autohantigEN [Homo sapiens], full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                           282 GluLys-----AspProValTrpLysLysLeu
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HTC; CAP trapper.
Mus musculus (house mouse)
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Gossypium raimondii
Gossypium raimondii
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
I (baess 1 to 816)
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    816 bp mRNA linear EST 16-JUN-2004
Eb Gossypium raimondii cDNA clone GR_Eb013122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 AlaLeuGlyLysGluGluGluGlyLysLysArg---LeuGluGluHisAspLysLysIle 185
                                                                                                                                                                                                                                                                                                                                                                  226 LeuGlyPhelysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLys 245
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                                                                                                                                                                                                                                                                        206 AlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGln 225
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  147 LeulysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLys 166
                                                                                                                                                                                 186 GluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAla 205
                                                                                                                                                                                                                                                                                                                     637 CTGAAG------CTAAAGGAAGCCCTCGAGAAAGAGGTTGGGATCATGAAAGCCAGC 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 GlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe
                            -----GAGGAGCTGAGGAGTAAGCAGAGGTGTCTGGAGCGCGAGCAGCAGACGGTG
                                                                                                                                                                                                                           577 AGCCAGCTTCAGCAGCTGCTGGAGAATCAGAAGAACTCCTCGGTGACCCTGGCGGACACC
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3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                Submitted (10-701-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Please visit our web site (http://genome.gsc.riken.jp/) for further
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/dev_stage="11 days embryo"
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, P., Hayatsu, M., Hiramoto, K., Hiracka, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sato, C., Sakai, K., Sano, H., Sasaki, D., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muzamatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshino, M., Muzamatsu, M. and Hayashizaki, Y.
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/db xref="taxon:5759"
/db xref="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
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Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Ilark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@cigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seg primer: M13-Forward
Class: shotgun
High quality sequence start: 7
High quality sequence stop: 852.
                                                                                                                                                                                                                                                                                                                                                                                889 bp DNA linear GSS 14-NOV-2000
Entamoeba histolytica Sheared DNA Entamoeba histolytica
----AAGAGACAAAGAGGCAAAGGAGAAG 726
                                                                                GlyLeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSer 330
                                                                                                                  AsnLysLysAsnArgllelleLysProLeuArgAsp-----LyslleGlyLysTyrThr 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Entamoebidae, Entamoeba.

1 (bases 1 to 889)
Loftus, Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:1MSS sheared DNA library
Unpublished (2000)
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Matches:
Conservative:
Mismatches:
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/strain="HM1:IMSS"
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   www.genoscope.cns.fr)
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62
50
88
70
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|db_xref="texon:99883"
|/tissue_type="Liver"
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Matches:
Conservative:
Mismatches:
Indels:
(E-mail : seqref@genoscope.cns.fr - Web
The sequences are based on single pass r
More information available at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       US-10-724-972A-6352 (1-335) x CR650378 (1-1483)
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116.00
41.48%
22.96%
6.86%
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Best Local Similarity:
Query Match:
DB:
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Direct Submission
Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
    |||||||||||::
| AATAAGAAGAATAAAGGGATTAAAATGGAGAAAAAAATTCAAAAGAAAACAAAATTCAAAAGAAAAA
                                                                -----ACTATAAGTCCA
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326 AGGATGAGGGTTAGGAACAGAATTAAAACAA---AATAAAGAAGTAGAAGAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGly
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                                                                                                        IlelleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaPro
                                                                                                                                                                   144 Thrile------GluLeuLysSerPheAspGlyAspTyrAsnGluAsnIle
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                                                                                                                                                                                                                                                             AGAAAGATAGAAGAATTACAAAAGAATTTAGAGTTAGAACAAGAACAAAAAAATCAACTT
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CR650378.1 GI:51146823
HTC; cDNA; full-length; Tetracdon nigroviridis
Tetracdon nigroviridis
Eukaryota: MATC-
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                                                                                                                                        ------GAAATCGTAGA------
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CR650378
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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576

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627

141 747

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BW253010 BR253010 684 bp mRNA linear EST 09-NOV-2002 BW253010 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb094pl5 5', mRNA sequence.
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Bukaryota, Metazoa, Chordata, Urochordata; Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.

1 (bases 1 to 684)
Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.

Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GAGGAAAAGGAGGTAAAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 ACAAAGTTCATTGAAGAAAACAGAGAGAAGTTTACTCAGTTGGACTTACAAGATGTTGAC 425
                                                                                       160 AlaPheLysThrIleSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGlu 179
                                                                                                                                                                                                                                                                  200 ValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrVal 219
                                                                                                                                                                                                                                                                                                                                                          220 GlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGly 239
                                                                                                                                                                                                                                                                                                                                                                                                                                               240 LeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnVal 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 GluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsp 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 IleLeuAspArgAspLeu-----TrpAlaArgSerArgGlyLeuIleSerSerGlu 316
                                                                                                                                                                                                                                                                                                                                                                                                   271 ------AAGCAGAAGGAGAAAGGAAGAAGAGAGAGCTAAAAGATGTTATGGATAGT 224
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                                                                                                                                                                             180 GluHisAspLysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLys
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  142 AlaProThrileGlu-----LeuLysSerPheAspGlyAspTyrAsnGluAsnIleAsp
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310 ATTATTACTGAGGAAACAAATAAGAAGGATCTGCTGGAA------
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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/organism="Ciona intestinalis"
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Department of Zoology
Kyoto University
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                                                                                                                               AL854856 AGC-egg Xenopus tropicalis cDNA clone TEGG004£24 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinxton. Cambridgeshire, CBIO 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEGG004f24.qlkT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
CDNA was oligo dT primed from Sug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site l: ECORI; Site_2: NotI
Host: Escherichia coli XL1-blue.
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                                                                                                                                                                                                                                                           Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Bukaryota, Metazoca; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota a tracchia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 673)
1 (Coning,M.D.R., Ashurat,J.L., Taylor,R., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22875075.
Contact: Taylor the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pc3107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pcS107 with EcoRI at the 5' end and NotI at the 3' end"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
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60
42
106
51
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Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus tropicalis"
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/db_xref="taxon:8364"
/clone="TEG9004f24"
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Indels:
                         AAGGTGTGCAACCCCATCATCACAAGATG 1185
Lys-----AspProValTrpLysLysLeu 290
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                                                                                                                                                                          sequence.
ALB54856
ALB54856.2 GI:38630328
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115.50
39.38%
23.17%
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Best Local Similarity:
Query Match:
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SM Ciona intestinalis
SM Ciona intestinalis
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
E I bases 1 to 690)
S Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)
L Unpublished (2002)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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127 CAATCCCAAATATTCACCACTTACTCGGACAACCAACCAGGTGTGTTGATCCAAGTGTAC 186
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355 AAGATCACAATCACCAACGACAAAGGTCGTCTTAGCAAAGAAGAAGATTTGAGCGGATGGTG 414
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                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole animal"
/dev stage="tailbud embryo"
/clome_lib="Nori Satoh unpublished cDNA library, tailbud
embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 ATCCCCCCTGCACCTCGTGGAGTTCCACAGATTGAGGTG---ACGTTCGATATGGTT
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                         Email: satoh@ascidian.zool.kyoto-u.ac.jp
Location/Qualifiers
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/organism="Ciona intestinalis"
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/db_xref="taxon:7719"
/clone="citb073p02"
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BW254793
BW254793.1 GI:24834711
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnGlu-----AsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGlu 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 GACGAAGATAAATCAGCGATTCTTAACAAAGCTAAAGAAGTTTTGGACTGGTTGGAAAAT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AlaproThrileGluLeuLysSerPheAspGlyAspTyr 154
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491 ------CTTAAATCAACAGTGGAGGATGACAAAGATAAAATTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 AACGAAGCCGAGAAATATAAGGAAGAA-----GATGAGAAGCAGAAG-----GAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             596 AACCAG------ACTGCCGAAAAGGACGAATATGAATTCCAACAAAAAGAACTT
                                                                                                                                                                                                                                                                                           AsnArgllellelysProLeuArgAspLysileGlyLysTyrThrSerValGlyThrArg
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|GAGAAAATTGCCAACCCTATTATGACAAAACTT 676
                                                                                                                                         Indels:
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                                                                                                                                                       Gaps:
                                                                 0.0259
115.50
41.04%
25.90%
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Best Local Similarity:
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DB:
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                 ORIGIN
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	Qy 183 LysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuPro 202 bb 417 AACGAAGCGAGAAATATAAGGAAGAAGATGAGAAGCAGAAGGATGAGAAGCAGAAGGAGAAGAAGAAGAAGAAGAAGAAGAAGA	SULT 30 23.942 CUS CUS BW235.942 CUS BW235.942 CUS CUS BW235.942 CUS SINTION BW235.942 CUSSION	Kyoto University Sakyo-tu, Kyoto, Kyoto 606-8502, Japan Sakyo-tu, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081 Fax: 81-75-753-4081 Fax: 81-75-705-1113 Email: satch@ascidian.zcol.kyoto-u.ac.jp. Location/Qualifiers Location/Qualifiers Lo
Oy 223 LeuSerGlnLeuGlyPheLyGGluAlaLeuSerAspAspValThrLyGGlyLeuSer 241	RESULT 29 BW222839 LOCUS BW222839 LOCUS BW222839 LOCUS BW222839 LOCUS BW222839 Nori Satch unpublished cDNA library, larva Ciona intestinalis cDNA clone cilv051j23 5', mRNA sequence. ACCESSION BW222839.1 GI:24742218 KEYWORDS Ciona intestinalis ORGANISM Ciona intestinalis CRANISM Ciona intestinalis CORGANISM Ciona intestinalis AUTHORS SACOU, Y., Shin: i.T., Kohara, Y. and Satch, N. TITLE TITLE TITLE DEPARTMENT Contact: Nori Satch COMMENT DEPARTMENT Contact: Nori Satch COMMENT DEPARTMENT CONTACT: Satch Kyoto University SAKVO-ku, Kyoto	Tel: 81-75-75-4081 Fax: 81-75-75-1113 Fax: 81-75-75-1113 Fax: 81-75-75-1113 Fax: 81-75-75-1113 Fax: 81-75-75-1113 Fax: 81-75-75-1113 Fax: 81-75-75-1113 Fax: 81-75-75-1113 Fax: 81-75-75-1113 Fax: 81-75-75-113 Fa	2A-6352 (1-335) x BW222839 (1-692) 9 ValAspAlaLeuValAlaLeuAspValLySProValGlyI

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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

SI (bases 1 to 702)

SI Satou; Y., Shin-i,T., Kohara,Y. and Satoh,N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished (2002)

Contact: Nori Satoh

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Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 GGAGGAGTGATGACAGCTTTG-----ATCAAGAGAAACACGACCGTCCCAACCAA 118
                                                                                                                                                                                                             /mol_type="mRNA"
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Conservative:
Mismatches:
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362 AAGATCACAATCACCAACGACGAAGGTCTTAGCAAGGAAGAAGATATTGAGCGGATGGTG 421
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                                                                                                                                                                                                                                                                                                                                  AsnArgHisLysGlyIleTyrLysAspLeuAsnLysIle------141
                                                                                                                                                                                                                                                                                                      134 CAATCCCAAATATTCACCACTTACTCGGACAACCAACCAGGTGTGTTGATCCAAGTGTAC 193
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                                                                                                                                                                ValAspalaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLys
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BW055754 Nori Satoh unpublished cDNA library, blood cells Ciona intestinalis cDNA clone cibd084g20 5', mRNA sequence.
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                                                                                                         155 AsnGlu-----AsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGlu 172
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Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 753)
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                                                                                                                                319 AACGGTATCTTGAATGTATCTGCT-----GTTGACAAGAGCACTGGAAAGGAGAAT
202 GAGGGTGAACGTACGATGACCAAGGACAACAACATACTTGGTAAGTTCGAGCTCTCCGGC
                                     -----AlaProThrIleGluLeuLysSerPheAspGlyAspTyr
                                                        517 -------CTTAATCAACGGGGGGGATGACAAGTGAAAGATAAATTTCA
                                                                                                                                                                               173 Glu-------GlyLysLysArgLeuGluGluHisAsp--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 GACGAAGATAAATCAGCGATTCTTAACAAAGCTAAAGAAGTTTTGGACTGGTTGGAAAAT
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Expressed genes in Ciona intestinalis (2002)
Unpublished (2002)
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Department of Zoology
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Ciona intestinalis
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/tissue_type="whole animal"
/dev stage="juvenile"
/clone_lib="Nori Satch unpublished cDNA library, juvenile
whole animal"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Ciona intestinalis
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona
1 (bases 1 to 713)
Satou, Y., Nakayama, A., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2004b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 AsnArgllelleLysProLeuArgAspLyslleGlyLysTyrThrSerValGlyThrArg 108
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                                     261
 242 LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro
                                                                       539 GACGAAGATAAATCAGCGATTCTTAACAAAGCTAAAAGAAGTTTTGGACTGGTTGGAAAAT
                                                                                                         262 GluargMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu
                                                                                                                                           599 AACCAG------ACTGCCGAAAAGGACGAATATGAATTCCAACAAAAAGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspLysLys
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CAATCCCAAATATTCACCACTTACTCGGACAACCAACCAGGTGTGGTTCCAAGTGTAC
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Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
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Indels:
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647 GAGAAAATTGCCAACCCTATTATGACAAAACTT 679
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/organism="Ciona intestinalis"
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BW441129.1 GI:48494172
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127 AspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGlu 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GAGGAGCTGAGGAGTAAGCAGAGGTGTCTGGAGCGCGAGCAGCAGCAGCAGTG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAla 205
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 981)
                                                                                                                                                                                         can
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                                                                                                                                   Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11646 row: c column: 07
High quality sequence start: 51
High quality sequence store: 51
High quality sequence store: 550.
Location/Qualifiers
                                                                                                                           M. Fatima
                         INTH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                           Contact: Robert Strausberg, Ph.D.
Bmall: Gapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
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    .981
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="CZECH II"
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115.50
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603167626F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5255742 5',
B1905625
B1905625.1 GI:16168168
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                            522 AAGATTCAAGCGAAGAACGGTCTCGAATCTTATGCGTTCAAC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro
                                                                                                                                                          ValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLys
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                   753
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                              Matches:
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264

	Percent Similarity: 38.55 Best Local Similarity: 23.28 Query Match: 6.83\$	DB: 9 IIS=10-724-972h-6352 (1-335) *	sAsnArg1]	Db 3067 AAGGCAGACGTCTC	107	Db 3127 AGCGAGAGAGAAG Qy 127 AspAspAsnArgHis	Db 3187 CAAAATCTTGCAG	147	Db 3226 GTGGAGGCTCTGAAA Qy 167 AlaLeuGlyLySGlu	3274	Qy 186 GluGluTyrLysLys	Db 3325 AGCCAGCTTCAGCAG	Qy 206 AlaLysSerGlyLeu	3385	226	3436	Qy 246 GlyProTyrLeuGln	266 IleMetThr	Db 3517	Qy 286 ValTrpLys	Db 3544 GTCGTCGACATGTCG	Qy 295AsnGlnArgVal	Db 3604 TTAAATGACAAACTG	Qy 314 SerSerGluGluMet	Db 3664 TCTGCCAAGGAC	Qy 334 AsnLys 335	Db 3721 CAGAAG 3726	RESULT 36 CR426562 LOCUS CR426562 CR426562		
AlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGln	424 CTGAAGCTAAAGGAAGCCCTCGAGAAAGAGTTGGGATCATGAAAGGCCAGC 474 226 LeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLys 245		GlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe	leMetTh	:::	ValTrpLysLeuAsnAlaValLys	GTCGTCGACATGTCGAAGTACAAAGCCACCAAGAACGACTTGGAGACCCCAGATTTCCAAC	295AsnGlnArgValAspileLeuAspArgAspLeuTrpAlaArgSerArgGlyLeu11e 313 	SerSerGluGluM	703 TCTGCCAAGGACGAGAAGGAGCTGCTCCACCTGAGCATCGAGGAGATCAGGGAC 759 ·	334 AsnLys 335	760 CAGAAG 765 .	AY420059 4107 bp DNA linear GSS 12-DEC-2003	Mus musculus HCM7097 gene, VIRTUAL TRANSCRIPT, partial sgenomic survey sequence.	AY420059 AY420059.1 GI:39776016			mammala, burnella; kodenta; sciulognachi; mulldae; muls. 1 (bases 1 to 4107) Clark A.G., Glanowski.S., Nielson.R., Thomas.P., Kejariwal.A.,	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,	Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous	geme LILOB Science 302 (5652), 1960-1963 (2003)	110/1302 Classes 1 to 4107) Clark A G Glannaski S. Nielson P. Thomas D. Kejariwal A.	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.	Adams, M.D. and Cargill, M.	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	NOCAVILE, NO 20030, USA This sequence as made by sequencing genomic exons and ordering them hased on alterment		org/ /mol/ /mol/	/locus_rag="HCM7097"	
	a &	qq	ò f					., S 43			& f		RESULT 35 AY420059 LOCUS	DEFINITION	ACCESSION VERSION	KEYWORDS	ORGANISM	REFERENCE		TITLE	JOURNAL	REFERENCE		4	JOURNAL	COMMENT	FEATURES		ORIGIN	

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-CTAAAGGAAGCCCTCGAGAAAGAGGTTGGGATCATGAAAGCCAGC 3435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    785 bp mRNA linear EST 17-JUN-2004
lbud Xenopus tropicalis cDNA clone TTbA033p07 5',
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CAGCAAGCAGCTGAACGTCCCAAAGTACAGCGACGTGAAG 3126
                                                                                                                                                                                                                            GAAG------CAGCCGGTCCCGCTGGAGCAG 3225
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|GACGGAGGTTCAGACCACCAAGCAG----- 3516
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                                                                                                                                                                                                          oAsnieuGluGlulleSeriysLeuLysProAspieullelleAla 126
                                                                                                                                             ellelysProleuArgAspLyslleGlyLysTyrThrServalGly 106
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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CR731171

Tetraodon nigroviridis full-length cDNA.

CR731171.

GR731171.

GR731171.

HTC; cDNA; full-length; Tetraodon nigroviridis.

Tetraodon nigroviridis

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontoidea; Tetraodontidae; Tetraodontiformes;

I (bases 1 to 1120)
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236 ValThriyaGlyLeuSeriyaTyrLeuLyaGlyProTyrLeuGlnMetAanThrGluThr 255
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TACTCCGAGTCCCTGAAGGACGCCCAGGAGAAGCTGGAGGAGGAGGAGAAGAAGGCAGCA 341
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Direct Submission

Submitted (10-A004) Genoscope - Centre National de Sequencage

2 rue daston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

More information available at

http://www.genoscope.cns.fr/tetraodon.
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                                                          216 AsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 AGGAAAGAAATCAGTTTTGAAAAGTATGCAAAAAGCCTAACAGCACTGCTGAGGAGCGA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 AsnileAspAlaPheLysThrileSerLysAlaLeuGlyLys---GluGluGluGlyLys 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThrMetAsp 195
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/clone=iba-XGC-tailbud"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from Sug of poly 4+ RNA from tailbud.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
                  Xenopus tropicalis (western clawed frog)

Bukaryota iropicalis (hordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Amphibias; Xenopous; Silurana.

(bases 1 to 785)

Croning, M.D.R., Ashurat, J.L., Taylor, R., Garrett, N. and Rogers, J.
                                                                                                          croning, M.D.R., Ashurst, J.L., Taylor, R., Garrett, N. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (2004)
                                                                                                                                                                               Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Bmail: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TTDA033p07.plkSp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
Seq primer: SP6.
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Mismatches:
Indels:
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Matches:
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GTGGACAAAAGCACTGGCAAAGAAAAAAAAGATCACCATCACCAATGACAAAGGTCGTCTC 1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluLeuLysSerPheAspGlyAspTyrAsn-----GluAsnIleAspAlaPheLysThr 163
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Mismatches:
Indels:
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Matches:
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HTC; cDNA; full-length; Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodont.
                                                                                           154 TyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAlaLeuGlyLysGluGlu--- 172
                                                                                                                                                                                                                                                                                                                                                                                                                         257
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                                                                                                                                                            ------GluGlyLysArgLeuGluGluHisAsp 182
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GATGCGGAGGCGGACGTGCTCTCTGAACCGGCGGATCCAGCTGGTGGAGGAGGAGCTG 401
                              AsnLysIleAlaProThrIle------GluLeuLysSerPheAspGlyAsp 153
                                                                                                                                                                                                                                                                                         198 GlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSer 217
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Direct Submission

Submitted (10-4004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Frb sequences are based on single pass reads.

More information available at http://www.genoscope.cns.fr/http://www.genoscope.cns.fr/tetraodon.
                                                                                                                275 GluProSerLeulysGluLeuGluLysAspProValTrpLysLysLeuAsnAlaValLys
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642 GAGGAACGCGCCGAGGCCGAGGCCAAATCTGGAGATCTT--------
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                                                                                                                                                                                           522 AAGATGGAGATCCAGGAGATGCAGCTGAAGGAGGCCAAGCACATCGCCGAGGAGGCCGAC
                                                    GACCGGGCCCAGGAGCGACTGGCCACGGCCCTCCAGAAGCTGGAGGAGGCCGAAAGCT
                                                                                                                                                                                                                                                                                                                                                         218 TyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThr
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/mol_type="mRNA"
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CR685229
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
IMPORTANT: this sequence may contain errors. The Ciona intestinalis
library from which the clone was isolated may be contaminated with
cDNAs from bacteria or other Eukarya.
Stazione A.Dohrn, Naples, Italy, and was prepared in
pBluescript28K+.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL666132 AL666132 ALF DP MRNA linear EST 11-JAN-2002 AL666132 directional larval cDNA library Ciona intestinalis CDNA clone 002ZE10 5', mRNA sequence.
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                                                                                                                                             183 LysLysIleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuPro 202
                                                                                                                                                                                                                                                                                                                                                                                      242 LysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnPro 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 GluargmetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeu 281
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                                                                                                                                                                                                                          203 AlavalAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPhe
                                                                                                                                                                                                                                                 456 ---GTGTCTGCAAAGAATGGCCTGGAGTCCTTTCAAC---------
                                                                                                                                                                                                                                                                                                                                             -------ATGAGTCAACTGTGGAGGATGAGAAGCTTGCTGGCAAGATCAGT
                                                                                                                                                                                                                                                                                                       223 LeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGly---LeuSer
                                                                                                      348 AAAATCACAATCACTAATGACAAAGGTCGTCTTAGTAAAGAGGACATTGAGCGCATGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciona intestinalis directional larval cDNA library Unpublished (2002)
                                                              173 Glu-----GlyLysLysArgLeuGluHisAsp
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 GluLys-----AspProValTrpLysLysLeu 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            648 GAGAAAGTATGTAATCCCATCATCACCAAACTG 680
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Phlebobranchia, Cionidae, Ciona.
1 (bases 1 to 711)
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Oryzias latipes

Oryzias latipes

Oryzias latipes

Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Meopterygii; Teleostei; Buteleostei; Necteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyidae; Oryziase.

I (bases 1 to 70;)

E Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.

Medaka EST Project in Takeda's lab

Unpublished (2001)

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Tel: 81-559-81-685

Email: tshini@genes.nig.ac.jp.

Logatin/Qualifiers
                                                                                                                      BJ706325 MF01FFA CDNA Oryzias latipes CDNA clone MF01FFA017e14 5', mRNA sequence.
BJ706325 GI:45247204
                             1881 GAGTACGAGCATCAGCAGAAGGAGCTGGAGAAGGTGTGCAACCCCATCATCACAAAGATG 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 GGTGGGGTGATGACGAGTCTTA-----ATCAAACGCAATACTACCAACAA 119
      273 SerAsnGluProSerLeuLysGluLeuGluLys-----AspProValTrpLysLysLeu 290
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AUTHORS
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ALIGNMENTS

APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH03-16
CURRENT APPLICATION NUMBER: 108/10/724,972A
CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: 09/450,969
PRIOR FILING DATE: 1999-11-29 Sequence 2580, Application US/10724972A Publication No. US20040147734A1 GENERAL INFORMATION: US-10-724-972A-2580

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APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
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APPLICANT: Younguth, R.
APPLICANT: You will be the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the propertion of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the pro
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
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Matches:
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Mismatches:
Indels:
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                    PRIOR APPLICATION NUMBER: 09/134,001
PRIOR FILING DATE: 1998-08-13
PRIOR PELING NUMBER: 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-68-14
NUMBER OF SEQ ID NOS: 7544
SEQ ID NO 2580
LENGTH: 1008
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Pred. No.:
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රු සි	5 ValA 1 GTGA	ValArgGlyLeuLysIleLeuŚerValIleGlyLeuLeuPheValLeuIleAlaThrAla 	eulysileLeuServalileGlyLeuLeuPhevalLeulleAlaThrAl 	LeuPhe TTGTTT	ValleuileAla 	Thrala 24 ACTGCA 60			GENERAL INFORMA APPLICANT: HAE APPLICANT: ON
È	25 AlaC	AlaCysGlyAsnAsnSerSerAsnSerSerIvsGluSerSerLysAspGlyValGlu	SerAsnSerSerLys	Gluser	SerLysAspGly				
ପ୍ଧ	61 GCAT	GCATÓTGGAAATAATAGTTCAAGTAAGTCAAGTAAAGAGTCATCAAAAGATGGAGTTGAA	AGTAACTCAAGTAAA	GAGTCA	TCAAAAGATGGA	 GTTGAA 120	0	Z Z Z	APPLICANT: Ca APPLICANT: Ya
රි සි	45 IleL 121 ATCA	IlelyshisGluGluGlyThrThrLysValProlyshisProlysArgValValValLeu 	ThrLysValProLys: 	Hispro 	LysArgValVal' AAACGTGTTGTT	Valleu 64 GTTCTT 180	0		AFFLICANT: XU TITLE OF INVEN TITLE OF INVEN
& 8	65 GluT	GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlylleAlaAsp 	LeuValAlaLeuAsp 	VallyB	ProvalGly11e			552	CURRENT APPLIC CURRENT FILING PRIOR APPLICAT
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È	125 IleA]		LysGly1leTyrLys	Aspleu	AsniysileAla) 4r	, , , , , , , , , , , , , , , , , , ,	
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& 90	145 IleGl	IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIle		\anile/	AspAlaPheLys7	Thrile 164	4 1 (, SC ; SEQ	NUMBER OF SEQ SOFTWARE: Fast SEQ ID NO 8156
ò	165 SerLy	SerLysAlaLeuGlyLysGluGluGluGlyLy	3luGluGlyLysLysA	rgleuc	sArgleuGluGluHisAsply				LENGTH: 1014 TYPE: DNA ORGANISM: Sta
Dp	481 TCAAA		3aagaaggtaaaaaac	GCTTAC]] 4AGAAA 540		Б Х,	FEATURE: NAME/KEY: CDS
ර සි	185 IleGl	IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVa 		snGlnI	BAsnGlnLysValLeuProAlaVal		-H	л ; US-09	LOCATION: (1) -09-815-242-815
3 8		AGAA IA IAAAAAAGAA	ATAACTATGGATAAA	ATCAM	AGGTATTGCCTG			Align Pred.	Alignment Scores: Pred. No.:
S 8		Aldarduyasetviyleelleellalahiseroseraanseriyvaldiydiinbhelesser 	ATAHISPIOSEIASEE 	CTTATO	/alGlyGlnPher 	LeuSer 224		Score: Percen Best L	Score: Percent Similarity Best Local Simila:
ò	225 GlnLe	GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu	JeuSerAspAspValT	hrLysG	lyLeuSerLysT	YrLeu 244		Query DB:	Match:
QQ .		caactaggttttaaagaagcattaagtgatgatgttactaaaggtttaagtaag	rtaagrgatgita	CTAAAC	GTTTAAGTAAGT	PATCTT 720		US-10	US-10-724-972A-63
දු දු	245 LyBG1 721 AAAGG	LysG1yProTyrLeuG1nMeTAsnThrG1uThrLeuSerG1nVa1AsnProG1uArgMet 	AsnThrGluThrLeus	erglnv 	/alAsnProgluA 	ArgMet 264		જે ક	1 G1X
ò	265 Pheil	PhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAsp	erSerAsnGluProS	erLeul	ysGluLeuGluL			8 8	
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දු පු	285 Prova 841 CCTGT	ProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArgAsp 	NaValLysAsnGlnA	rgvala 		rgasp 304		λ i	
ò	305 LeuTrpAl	TALARA	eulleSerSerGluG	Tumer a	Viio,TirlSov,Tell			g ;	
qa				AAATGG	CAAAAGAACTTG			à 4	51 VAL ::: 199 ATC
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3		Innganagainginada	AAGATAATAAG 993					QQ	259 ĠĠŢŹ

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| STATES | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972 | 1972
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Alignment Scores:
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APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
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APPLICANT: Trawick, John
APPLICANT: Parmamotor, Robert
APPLICANT: Yamamotor, Robert
APPLICANT: W. H.
APPLICANT: N. H.
APPLICANT: Xu, H.
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APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: N. H.
APPLICANT: NUMBER: 0503-02-20
CURRENT PILING DATE: 2003-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
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                                                                                                                                                                                                                                                                                                                                                 ProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGlu 280
                                                                                                                                                                                                                                                                                                                                                                                             LeuGluLysAspProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIle 300
                                                                                                                                                                                                                  LeuProhlaValhlahlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGly 220
                                                                                                                                                                                                                              GINPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 240
                                                                                                                                                                                                                                                                                                      SeriysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsn 260
                                                                                                                                           IlealaProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAla 160
                                                                                                 PhelysthrileSerLysAlaLeuGlyLysGluGluGluGlyCysLysArgLeuGluGlu
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                                         ProAspieullelleAlaAspAsnAsnArgHisiy8GlyIleTyrLysAspleuAsnLys
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            GlubeuValGlubeuSerbysbysAspSerbys 331
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Publication No. US20040029129A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
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105 ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SeriyaalahenGlyiyaGluGluGluGlyGyvsiyaArghenGluGluHisAapiysIvs 184
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 78614
SEGMAINING PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
SEGMANE: PARCHILIN VETRION 3.1
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Best Local Similarity:
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61 GAATCATCAACTAAAGATACTATTTCGGTAAAAGATGAAAATGGTACAGTACAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 ValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThrGluThr 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuSerGlnValAsnProGluArgMetPhelleMetThrAsnLysAlaSerSerAsnGlu 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 LysGluSerExerLysAspGlyValGluIleLysHisGluGluGlyThrThrLysValPro
                                                                                                  16 LeuLeuPheValLeuIleAlaThrAlaAlaCysGlyAsnAsnSerSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 ProSerLeutysGluteuGlutysAspProvalTrpLysLysLysLysLyslen
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                                                                       US-10-724-972A-6352 (1-335) x US-09-815-242-4404 (1-927)
             Conservative:
Mismatches:
Indels:
Gaps:
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          85.11% 72.82% 69.88% 9
      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-815-242-4194
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US-09-815-242-4404

Sequence 4404, Application US/09815242

Sequence 4104, Application US/09815242

Sequence 4104, Application US/09815242

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, M. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITAN, 011A
CURRENT APPLICATION NUMBER: 06/191,078

FILE REFERENCE: ELITAN, 011A
CURRENT PAPLICATION NUMBER: 60/200,727

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

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PRIOR PILING DATE: 2000-11-27

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Pro---ValTrpLygLygLysLeuAsnAlaValLysAsnGlnArgValAsplleLeuAspArg 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyproTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe 265
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595 TCAAGAGCAGGTATGTTATTATTAATGAAGATACATTTATGGGACAATTCTTAATAAA
                                                                           146 GluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSer
                                                                                                                                                                        166 LysalaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLyelle
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186 GluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAla
                                                                                                         Essential Genes in
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TITLE OF INVENTION: Identification of EBSenti
TITLE OF INVENTION: Identification of EBSENTI
TITLE OF INVENTION: DECKARYOTES
TITLE OF INVENTION: DECKARYOTES
TITLE OF INVENTION: DATE: 2010
CURRENT FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Trawick, John D.
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US-09-815-242-8024
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                                                                                                                 APPLICANT: HEBELDECK, NOWELL APPLICANT: Oblian, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramico, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
ITTLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: OF ELITRA.011A
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-26
PRIOR PILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
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Matches:
Conservative:
Mismatches:
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                      Sequence 4194, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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ORGANISM:
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Alignment Scores:
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                                                                                                                                                                                                    ArgGlyLeuLysIleLeuSerValIleGlyLeuLeuPheValLeuIleAlaThrAlaAla
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 8024
LENGTH: 960
TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE: NAME/KEY: CDS
ILOCATION: (1)...(960)
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65.85$
47.08$
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US-09-815-242-8024
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                                                                                                                                                                                                                                                                                                                            US-10-470-048B-301

Sequence 301, Application US/10470048B

Publication No. US20050037444A1

Publication No. US20050037444A1

APPLICANT: METNKE ET AL.

TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN

TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN

FILE REFERENCE: SONN:035US

CURRENT APPLICATION NUMBER: US/10/470,048B

CURRENT FILING DATE: 2003-07-25

NUMBER OF SEQ ID NOS: 603

SOFTWARE: Patentin version 3.1

SEQ ID NO 301

LENGTH: 957
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                                                                                                                    IleMetThrAsn---LysAlaSerSerAsnGluProSerLeuLysGluLeuGluLysAsp
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Conservative:
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Indels:
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yau, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 08/10/282,122A
CURRENT PILING DATE: 2008-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/201, 727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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730 AATGAAGAACTTGCCAATATCAATCCAAAAGTTATGATTTTAGCCACTGACGGAAAAACG 789
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                        HisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeu 232
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Wali
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Ohlsen, Kari
Zyskind, Judith
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2011-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 960
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US-10-282-122A-7949
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66.67$
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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APPLICANT: Mandio, Carlos
APPLICANT: Mandio, Carlos
APPLICANT: Mandio, Carlos
APPLICANT: Malone, Clerios
APPLICANT: Malone, Clerio
APPLICANT: Malone, Clerio
APPLICANT: Malone, Clerio
APPLICANT: Malone, Mari
APPLICANT: Mari
APPLICANT: Mandio, Carlo
APPLICANT: Mandio, Mari
APPLICANT: Persyth, R.
APPLICANT: Persyth, R.
APPLICANT: Persyth, R.
APPLICANT: Persyth, R.
APPLICANT: Persyth, R.
APPLICANT: Persyth, R.
APPLICANT: Presyth, R.
APPLICANT: Persyth, R.
APPLICANT: 2000-03-20
PRIOR APPLICANTION NUMBER: 60/200, 47
PRIOR APPLICANTION NUMBER: 60/200, 47
PRIOR APPLICANTION NUMBER: 60/200, 47
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2000-01-03
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PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-03-06
PRIOR APPLICANTION NUMBER: 60/25/930
PRIOR PILING DATE: 2001-03-06
PRIOR APPLICANTION NUMBER: 60/25/930
PRIOR PILING DATE: 2001-03-06
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PRIOR APPLICANTION NUMBER: 60/
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253 ThrGluThrLeuSerGlnValAgnProGluArgMetPhelleMetThrAsn---LysAla 271
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Gaps:
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Malone, Kari
APPLICANT: Apskind, Judith
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
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APPLICANT: Yamamoto, Robert
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APPLICANT: Yamamoto, Robert
APPLICANT: Yau, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: 00/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/200, 488
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-06
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487 CAGGATATTGCGGACATCGCCAAA-----ACGTTACCGAAAGGGAAAAAGGCGATTATC
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541 GGTGTTTCACGTGAAACCCAATTTAATTTATAATAGCGAATCCTATGCTGGTGGCTTA
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - S
NUMBER OF SEQ ID NOS: 79614
SEQ ID NO 30706
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LeuGluLysAspProValTrpLysLysLeuAsnAlavalLysAsnGlnArgValAspIle 300
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                                                                                     LeuAspArgAspLeuTrpAlaArgSerArgG]yLeuIleSerSerGluGluMetAlaLys
                                                                                                                                                                                                                           Sequence 2066, Application US/09974300
; Sequence 2066, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
    APPLICANT: Clausen, ID Groth
    TITLE OF INVENTION: Expression
    FILE REPERENCE: 10085.500-US
    CURRENT FILING DATE: 2001-10-05
    PRIOR FILING DATE: 2000-10-05
    PRIOR FILING DATE: 2000-10-06
    PRIOR FILING DATE: 2000-10-06
    RIOR FILING DATE: 2000-10-06
    RIOR FILING DATE: 2001-03-27
    NUMBER OF SEQ ID NOS: 8481
    SOFTWARE: FARENCE OF SEQ ID NOS: 8481
    SEQ ID NO 2066
    LENGTH: 801
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Matches:
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                                                                                                                                       321 GluLeuValGluLeuSerLysLysAspSerLys 331
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862 GAAGTCCAAGACTTTGTAACGAAATCCGCCAAA 894
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	Oy 230 GluAlaLeuSerAspA
	Db 62 AATGCATTAAGTGACG
	Qy 250 GlnMetAsnThrGluT
Db 657 AGACCGATCGAAAAGATCCTCTTTGGAAAAGCTCAGCGCAGTCAAAAAGGGCAGGTT 716	
Oy 299 AspileLeuAspArgAspLeuTrpAlaArgSerArgGlyLeuIleSerSerGluGluMet 318	Qy 270 LysAlaSerSerAsnG
319 Ala	290
ATA TT	
	Qy 310 ArgGlyLeuIleSerS
US-08-781-986A-355 ; Sequence 355, Application US/08781986A	Db 302 CGTGGCTTAATTTCTT
; Publication No. US20030054436Al ; GENERAL INFORMATION:	Oy 330 SerLys 331
; APPLICANT: Charles Kunsch ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Seguences	0b 362 CAAAAG 367
	RESULT 14
; ADDRESSEE: Human Genome Sciences, Inc. ; STREET: 9410 Key West Avenue	US-10-329-624-355 ; Sequence 355, Application US,
; CITY: Rockville	<pre>; Publication No. US2004004303' ; GENERAL INFORMATION:</pre>
COUNTRY: USA	; APPLICANT: Charles Kur ; Gil H. Choi
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COMPUTER: DISACTOR 48() 3.30 INCH, 1.4MD STORAGE COMPUTER: OPERATING SYSTEM: MSDOR COMPUTER: DISACTOR COMPUTER: DISACTOR COMPUTER: DISACTOR COMPUTER: DISACTOR COMPUTER: DISACTOR COMPUTER: DISACTOR COMPUTER: DISACTOR COMP	; Steven C. F
SOFTWARE: ASCII Texton over	; TITLE OF INVENTION: St. SOUGHCES:
APPLICATION NUMBER: US/08/781,986A	CORRESPONDENCE ADDRESS HUMAN
CLASSIFICATION: 435	; STREET: 9410 Key
HAPPLICATION NUMBER:	; STATE: Maryland
ATTOTION DATE: NAME: PARTINE DATE NAME: PART	ZIP: 20850
4	MEDIUM TYPE: Disk
KEFERENCE/DOCKET NUMBER: P8248PP; TELECOMMUNICATION INFORMATION:	OPERAING SYSTEM:
TELEFHUNE: (301) 309-8504 TELEFAX: (301) 309-8512	CURRENT APPLICATION DA
SEQUENCE CHAPACTERISTICS:	PRIOR APPLICATION NOTES :
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Alignment Scores:	ATTORNEY/AGENT INFORMA

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| 13.98-31 | Length: 668 |
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| 13.98-31 | Length: 618 |
| 13.98 | Conservative: 15 |
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| 13.91 | Conservative: 16 |
| 14.972.6132 (1-313) | Length: 686.135 (1-68) |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 GluhlaleuSerAppAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeu 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluMetAsnThrGluThrLeuSerGlnValAsnProGluArgMetPhelleMetThrAsn 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysalaSerSerasnGluProSerLeuLysGluLeuGluLysaspProValTrpLysLys 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 TIGAATGCAGTTAAAAATAATCGCGTGGATATTGTTGATCGTGATGTTTGGCAAAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgGlyLeuIleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 LeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLys
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91
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16
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Matches:
Conservative:
Mismatches:
Indels:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/POCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPAK: (301) 309-8439
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19870, Application US/10282122A publication No. US20040029129A1 GENERAL INFORMATION:
APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos APPLICANT: Malone, Cheryl APPLICANT: Haelbeck, Robert APPLICANT: Obskind, Judith APPLICANT: Trawick, John APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert AP
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                                                                                                                                                                                                                                                                                                                                                                                 1.95e-31
475.00
86.89%
74.59%
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Query Match:
DB:
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US-10-282-122A-19870
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165 SerlysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 IleAlaAspAsnAsnArgHisLysG]yIleTyrLysAspLeuAsnLysIleAlaProThr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspAsnLysLysAsnArg1le1leLysProLeuArgAspLys1leGlyLysTyrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp
  PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/245,793
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2010-10-29
PRIOR PILING DATE: 2010-01-20-9
PRIOR PILING DATE: 2010-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR SPRIOR APPLICATION NUMBER: 60/269,308
PRIOR SPRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR SPRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2010-02-06
PRIOR SPRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2010-02-06
PRIOR SPRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2010-02-06
PRIOR SPRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2010-03-06
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Matches:
Conservative:
Mismatches:
Indels:
2003-02-20
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460.00
57.09$
35.82$
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64

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104 249

Conservative: 62 Mismatches: 104 Indels: 16 Gaps: 4

Percent Similarity:	244	633 US-10-724-972A-6352 (1-3	263 Qy	693 DB 76	98 283 Qy 65 GluTyrSerPheValAspAl 1.	303	804 Db 1	323 Qy	864 Db 256	Oy 125 IleAlaAspAsnAsnArgHi	Db 316 ATTGCCGACAGCAGTCGCCA	Qy 145 IleGluLeuLysSerPheAs	Db 376 CTGCTGCTTAAGTCCCGCAA	Oy 165 SerLysAlaLeuGlyLysGlı	Db 436 GGCGAAATGGTGGTAAAAA	Qy 185 IleGluGluTyrLysLysGlu	Db 496 ATGGCGCAGTGGGCCAGCCACA	Qy 205 AlaAlaLysSerGlyLeuLe	Db 550 TCACGCGAACACCAATTCAAC		610	245	640 GCGGTGCGTCCATGC	264	Db 700 CTGCTGGTTGCCACTACTC		751	Ov 304 AspleuTroAlaArdSera		Qy 324 Gluleu 325	Db 871 AAATC 876		; Sequence 20621, Application US/10; Publication No. US20040029129Al; GENERAL INFORMATION: ; APPLICANT: Wang. Liangsu
::: ::: ::: TCACGCGAACACCTAGAACTTCAACCTTGCATACCCAGAACTTGCACACACA	euGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysfyrLeu	::: AACGTTCCCGCTGCGATG	LysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg	PMPTThrbart von 1 source and	Servanding to Serve	AspProvalTrpLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg		rpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuVal	GGGCGCGGATGCGCGCAGAGCGTATTGCCGCTGACGGTA									į	it cenes in														909 100
 CAACCTGCATACCCAG	uAlaLeuSerAspAsp		-GlnMetAsnThrGlu' ::: 	or contract of the contract of	9 1	Ā	sis	ArgGlyLeuIleSer	scecerarrrrecce				09815242		_		Ē	ų	tes	8/09/815,242	-21 191,078	206,848	727,727	242,578	253,625	257,931	269,308	•	Version 4.0				Length: Matches:
:: CACGCGAACAGCTATT	GlnLeuGlyPheLysGl	TCTCTGGGGCTG	LysGlyProTyrLeu GCGGGCGTCCATGCC	Met Phe I Jewet Thras	CTGCTGGTTGCCCACTATCGC	gpprovalTrpLysLys	GATCCGCTCTGGCAGATA		AACGCCTGGGCGCGGATC	GluLeu 325 ::::::	AAATC 870	6372	Application US/09815242 20020061569A1	ATION: selbeck, Robert	Ohlsen, Kari L. Zyskind, Judith W.	Wall, Daniel Trawick John D	Carr, Grant J. Yamamoto, Robert	tu, H. Howard	5	CATION NUMBER: U	G DATE: 2001-03-21 TION NUMBER: 60/191	TION NUMBER: 60/	PRIOR FILING DAIE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727	TION NUMBER: 60/	ATTING DATE: 2000-10-23 ATTING DATE: 20/253,625	DAIE: 2000-11-2/ TION NUMBER: 60/257,931	DAIE: 2000-12-22 TION NUMBER: 60/269,308 DATE: 2001-02-16	. 오 4	: Fabtsed for Windows Version 6372 909	cherichia coli) (909) 72	: 5.52e-30 460.00
Db 544 T	Qy 225 G	604	Qy 245 Ly Db 634 G(694	Qy 284 AE	Db 745 G	Oy 304 As	805	324	865	RESULT 16 US-09-815-242-63	; Sequence 6372, Appl ; Patent No. US200200	<u> </u>		, APPLICANT: W		2	TITE OF INVE	CURRENT APPLICATION	PRIOR APPLICA	PRIOR APPLICA	PRIOR APPLICA	PRIOR APPLICA	PRIOR APPLICA	PRIOR APPLICATION	; PRIOR APPLICATION PRIOR FILTNG DATE	NUMBER OF SEQ	SEQ ID NO	; TYPE: DNA ; ORGANISM: Escheric		; LOCATION: (1); US-09-815-242-6372	Alignment Scores: Pred. No.: Score:

)	t caps:
US-10.	-724-972A-6352 (1-335) x US-09-815-242-6372 (1-909)
ò	45 IleLysHisGluGlyThrThrLysValProLysHisProLysArgValValValLeu 64
qq	
ò	65 GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp 84
qq	136 GAACTCTCGTTCGCCGATGCCTTGGCCGCCGTCGACGTCATCCCGATCGGTATTGCCGGAC 195
ò	85 AspAsnLysLysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSer 104
qq	196 GATAACGATGCAAAACGCATCCTGCCCGAAGTGCGTGCGCACCTGAAACCGTGGCAGTCC 255
ò	105 ValGlyThrArgLysGlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIle 124
qq	256 GTCGGAACGCGCGCGCGCGAGCCATGCCGCTCTGAAACCAGGCCTGTGATG 315
δ	125 IleAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThr 144
qq	316 ATTGCCGACAGCGCTCGCCGTGCGGGGTTTACATCGCCCTTGCAGCAAATCGCGCCGGTA 375
λ	145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIle 164
QQ	376 CTGCTGCTTAAGTCCCGCAACGAAACCTACGCTGAAAATTTGCAATCTGCGGCTATCATC 435
ò	165 SerLysAlaLeuGlyLysGluGluGlyLysLysLysArgLeuGluGluHisAspLysLys 184
qq	436 GGCGAAATGGTGGGTAAAAAGCGAGAGATGCAGGCACGTCTGGAACAACATAAAAAAGAGG 495
λΌ	H
QQ	496 ATGGCGCAGTGGCCAGCCAGCTTCCCAAAGGGACACGCGTGGCCTTTGGCACA 549
δλ	205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
qa	550 TCACGCGAACAGCAATTCAACCTGCATACTCAGGAGACCTGGACCGGCAGCGTGCTGGCC 609
6	225 GlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu 244
q ₀	
δ	245 LysGlyProTyrLeuGlnMetAsnThrGluThrLeuSerGlnValAsnProGluArg 263
qq	640 GCGGGTCCGTCCATCGGCCTGGAGCAACTGCTGGCGGTCATCCTGCCTG
ò	AlaSer
QQ	700 CTGCTGGTTGCCCACTATCGCGAAGAGAGCATTGTTAAACGCTGGCAACAA 750
ò	284 AspProValTrpLysLysLysLeuAsnAlaValLysAsnGlnArgValAspIleLeuAspArg 303
Пр	751 GATCCGCTCTGGCAGATGTTAACCGCCGCAGAAGCAGCAGGTTGCTTCGGTCGACAGT 810
ò	304 AspLeuTrpAlaArgSerArgGlyLeulleSerSerGluGluMetAlaLysGluLeuVal 323
qq	811 AACACCTGGGGGGGGTATTTTTTTTTGCTGCAGAGCGTATTGCCGCTGACAGAGGTA 870
ò	324 GluLeu 325
qq	871 AAAATC 876
RESULT US-10-2 ; Seque ; Publi ; GENER	RESULT 17 15-10-282-122A-20621 Sequence 20621, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:

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700 CTGCTGGTTGCCCACTATCGC-----GAAGAGAGCATTGTTAAACGCTGGCAACAA 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 MetPhelleMetThrAsnLysAlaSerSerAsnGluProSerLeuLysGluLeuGluLys 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspprovaltrpLysLysLeuAsnAlavalLysAsnGlnArgvalAspIleLeuAspArg 303
                                                                                                                                                                                                                                                                                              reaceceaacaecaattcaacctecatactcaegaeaccteeacedecaeceteece 609
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   145 IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrile
                                             205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer
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TITLE OF INVENTION: NIMR COMPOSITIONS AND THEIR METHODS OF USE
FILE REFERENCE: PKZ-043
CURRENT APPLICATION NUMBER: US/10/893,671
CURRENT FILING DATE: 2004-07-15
PRIOR PRILING DATE: 2004-07-16
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-10
NUMBER OF SEQ. ID NOS: 98
SOFTWARE: Patentin Ver. 2.0
SEQ. ID NO 14
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 rcrcrddddcrg------
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TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PPLICATION NUMBER: 60/191,078
PRIOR PLLING DATE: 2000-03-21
PRIOR PLLING DATE: 2000-05-23
PRIOR PLLING DATE: 2000-05-23
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-09-06
PRIOR PLLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-12-22
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
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Forsyth, R.
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ORGANISM: Escherichia coli
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Best Local Similarity:
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APPLICANT: Xu, H.
TITLE OF INVENTION: A. H.
TITLE OF INVENTION: A. H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA 022.02.20
CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR APPLICATION NUMBER: 60/203-21
FRIOR PILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-26
FRIOR PELICATION NUMBER: 60/207,727
FRIOR PLILING DATE: 2000-05-06
FRIOR APPLICATION NUMBER: 60/207,30,335
FRIOR PLILING DATE: 2000-09-06
FRIOR APPLICATION NUMBER: 60/203,347
FRIOR FILING DATE: 2000-10-23
FRIOR PLILOR DATE: 2000-11-27
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45 IleLysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeu
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APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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GENERAL INFORMATION:
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328 TATAACGACCTGGCCTGGCTCCGACGCTGATGTTGCCGTCACGCGGGGGAGGACTAT 387
                                      AsnGluAsnIleAspAlaPheLysThrileSerLysAlaLeuGlyLyAgGluGluGluGly 174
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yallyakanGlnArgyal---AspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
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67 GGGAATTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 126
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TTCCAAAAA------GATGCAAAAGCAAAGTATAAAGATGCATGGAAA
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13 ATTAAAATGCTT----GTTGTTACGCTTGCTTTCCTACTTGTT----TTAGCAGGATGTAGT
                                                                                                                                48 GluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSer
                                          28 AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGluIleLysHis
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US-10-278-946-15
; Sequence 15, Application US/10278946
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Publication No. US20030153733A1 GENERAL INFORMATION:

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GENERAL INFORMATION:

TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: P8461USD1
CURRENT APPLICATION WUMBER: US/10/278,946
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 09/830,217
PRIOR FILING DATE: 1999-001-04-24
PRIOR APPLICATION NUMBER: US 60/078,682
PRIOR APPLICATION NUMBER: US 60/080,296
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN NUMBER: US 60/084,674
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 15
LENGTH: 999
THEND APPLICATION NUMBER: US 60/084,674
PRIOR FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 15

TYPE: DNA ORGANISM: Staphylococcus aureus US-10-278-946-15

Alignment Scores

Length:
Matches:
Conservative:
Mismatches:
Indels: 3.28e-25 405.00 51.74% 32.85% 23.96% Percent Similarity: Best Local Similarity: Query Match:

999 113 132 34

US-10-724-972A-6352 (1-335) x US-10-278-946-15 (1-999)

19 ATTAAAATGCTT---GTTGTTACGCTTGCTTTCCTACTTGTT---TTAGCAGGATGTAGT 72 LeulyglleLeuServalIleGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGly æ

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28 AsnAsnSerSerAsnSerSerLysGluSerSerLysAspGlyValGlulleLysHis 47

68 PheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLys 87 193 GCCACTGACGTCGCTGTATCTTTAGGTGTTAAACCTGTAGGTGCTGTAGAATCATGGACA

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88 LysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSerValGlyThr 107 ::: 253 CAAAAACCGAAATTCGAATACATAAAAATGATTTAAAAGATACTAAGATTGTAGGTCAA 312

148 LysserPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla 167

128 AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu 147

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TyrLysLysGlulleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys 207

881

221 GlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSerAspAspValThrLysGlyLeu 240 ------AATAAAGACTTA 690 241 SeriysTyrLeuLysGly-----ProTyrLeuGlnMetAsnThr---GluThrLeuSer 257 ||| | TTAGTTAAAAAGACTGAAAGGGAATGGACTTCAAGTAAAGAGTGGAAAAATTTAGACGGA 870 312 LeulleSerSerGluGluMetAlaLysGluLeuValGluLeuSerLysLysAspSerLys 331 258 GlnValAsnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSer Leu------LysGluLeuGluLysAspProValTrpLysLysLeuAsnAla -GATGCAAAAGCAAAGTATAAAGATGCATGGCCATTGAAA -SerTyrValGly SerGlyLeuLeuAlaHisProSerAsn-TTCCAAAAA-208 589 649 278 8 유 ò g ò 쉽 ò 요 양 g ò Ωp ò 임

332 іувАврАвпіув 335 ||| :::||| 985 AAACAATCAAAA 996

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RESULT 22
US-10-967-189-15
i Sequence 15, Application US/10967189
i Publication No. US20050053995A1
i GENERAL INFORMATION:
i TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
i TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
i TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
i FILE REFERENCE: PRAG1USD2
i CURRENT FILING DATE: 2004-10-19
i PRIOR PLICATION NUMBER: US 10/278,946
i PRIOR PELING DATE: 2002-10-24
i PRIOR PELING DATE: 2002-01-15
i PRIOR PELING DATE: 1999-03-18
i PRIOR PILING DATE: 1999-03-18
i PRIOR PILING DATE: 1998-03-0
i PRIOR PILING DATE: 1998-03-0
i PRIOR PILING DATE: 1998-04-01
i PRIOR PILING DATE: 1998-04-01
i PRIOR PILING DATE: 1998-04-01
i PRIOR PILING DATE: 1998-05-07
i NUMBER: OF SEO ID NOS: 22
i SOFTWARE: PatentIn version 3.1
i SEQ ID NO 15
i LENGTH: 999

ORGANISM: Staphylococcus aureus US-10-967-189-15 TYPE: DNA

999 1113 65 132 12 Length: Matches: Conservative: Mismatches: Indels: 3.28e-25 405.00 51.74% 32.85% 23.96% Percent Similarity: Best Local Similarity: Alignment Scores Query Match:

US-10-724-972A-6352 (1-335) x US-10-967-189-15 (1-999)

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811 Tragitaaaaagactgaaagcgaatggacttcaagtaaagagtggaaaatttagacgca 870
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                                                                               73 GGGAATTCAAATAAACAATCATCTGATAACAAAGATAAGGAAACAACTTCAATTAAACAT 132
                                                                                                                          48 GluGluGlyThrThrLysValProLysHisProLysArgValValValLeuGluTyrSer 67
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---TCTACTGATACAGTTTTCAAA-TTCAAA---GATACAACTAAGTTAATGGGGAAAGGT
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                   19 ATTAAAATGCTT---GTTGTTACGCTTGCTTTCCTACTTGTT---TTAGCAGATGTAGT
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LeulygileLeuServalileGlyLeuLeuPheValLeuIleAlaThrAlaAlaCysGly
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RESULT 23
US-08-781-986A-238
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; Sequence 23 y Application US/08781986A
; Sequence 23 y Los of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INFORMATION:
TELEPAX: (301) 309-8514
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 3775 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: double
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51,74%
32.85%
23.96%
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity:
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TOPOLOGY:
US-08-781-986A-238
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Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                     414
                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      973 TATAAATCTTCATTAAAACTTATTGACGATTTATATGAA-----AAGTTAAATATTGAA 1026
                                                                                                                                     LeuGlytysegluGluGluGlyDrystysArgLeuGluGluHisAspLysLysIleGluGlu 187
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583 TTCCAAAAA------GATGCAAAGCAAAGTATAAAGATGCCATTGAAA 630
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                                                                                                                                                                                                                                                                                                                                                    GlnValAgnProGluArgMetPheIleMetThrAsnLysAlaSerSerAsnGluProSer 277
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GAACCTGCACCTAAACTTAGAGGAAATCTCTAAATTAAAACCGGACTTAATTGTCGCGTCA
                                     AsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrIleGluLeu
                                                                                    LysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIleSerLysAla
                                                                                                           ---TCTACTGATACAGTTTTTCAAATTCAAA---GATACAACTAAGTTAATGGGGAAAGCT
                                                    TyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                                                                                                                                                                     SerGlyLeuLeuAlaHisProSerAsn---------SerTyrValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
UTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                    GAAATCTTAAATGATTTAGGATTCAAACGT-----
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STREET: 9410 Key West Avenue
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US-10-329-624-238
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---TCTACTGATACAGTTTTCAAATTCAAA---GATACAACTAAGTTAATGGGGAAAGGT
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Conservative:
Mismatches:
Indels:
                                                                                                                              APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/POCKET NUMBER: PB248PID1
TELECOMMINICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEPHONE: (240) 314-1224
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                           APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 238:
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3775 base pairs
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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Best Local Similarity:
Query Match:
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Query Match:
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 582
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523 TTAGGGAAAGAAAAAGAAGCTGAAGATTTACTTAAAAAGTACGATGATAAAGTAGCTGCA
                                                       TTCCAAAAA------GATGCAAAAGCAAAGTATAAAGATGCATGCATTGAAA
                                                                                                              GlnPheieuSerGlnLeuGlyPheiysGluAlaLeuSerAspAspValThrLysGlyLeu
                            188 TyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaValAlaAlaLys
                                                                                      ---SerTyrValGly
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-02-09
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
                                                                                         SerGlyLeuLeuAlaHisProSerAsn-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Cyskind, Judith
APPLICANT: Yskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Faryick, John
APPLICANT: Faryick, Robert
APPLICANT: Forsyth, R.
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|1027 AAACAATCAAAA 1038
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US-10-282-122A-9415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 GGACAGCAAAAAGGAGAAAAAAAAAAAAAAGGAAAATAAAAATCAAGCTATAACA 114
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PREMAINING PRIOR APPLICATION ALSO APPLICATION OF 160/2-16
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 9415
LENGTH: 972
                                                                                                                                                                                                                                                                                                                       972
1116
122
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Matches:
Conservative:
Mismatches:
Indels:
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391.00
51.93%
34.42%
23.14%
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Best Local Similarity:
                                                                                                                                                                                                                                                                 US-10-282-122A-9415
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_	Qy 104	Db 292	Oy 124	Db 352		Db 409	Oy 160	Db 469	Qy 180	Db 520	Qy 200	Db 577	Qy 220	0D da	Qy 240	Db 682	Qy 260	Db 736	Qy 279	Db 796	Qy 299	Db 856	Qy 318	Db 916	RESULT 27	Sequence 718:	; GENERAL INFO	; APPLICANT: 1; TITLE OF IN	CURRENT FILE PRIOR APPLIC	; PRIOR APPLIC	; NUMBER OF SE ; SOFTWARE: C.	; SEQ ID NO 716 ; LENGTH: 220	; TYPE: DNA	US-10-450-763-7
. Qy 230 GluAlaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeu 249	Db 691TTAACAAATACTTTTGAAGCAGGAAAATCTGAGCCTGATGGTTTCAAA 738	Qy 250 GlnMetABnThrGluThrLeuSerGlnValAsnProGluArgMetPheIleMetThr 268		Qy 269 ABRILYBALaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLys 288	Db 799 GATGAAGATAACATTTTTGACACGCAACTAAAAGGCAACCCTGCTTGGGAA 849	Oy 289 LysLeuAsnAlaValLysAsnGlnArgValAsplleLeuAspArgAspLeuTrpAlaArg 308	Db 850 GAATTAAAGTTTAAAAAGAAAACAAAATGTATAAATTAAAAGGCGACACTTGGATTTTC 909	Qy 309 SerArgGlyLeuIleŞerSerGluGluMetAlaLy8GluLeuValGluLeu 325		RESULT 26	US-09-974-300-2061 ; Sequence 2061, Application US/09974300	; Patent No. US20020146721A1 ; GENERAL INFORMATION:	; APPLICANT: Berka, Randy M. ; APPLICANT: Clausen, 1b Groth	; TITLE OF INVENTION: Methods For Monitoring Multiple Gene ; TITLE OF INVENTION: Expression	; FILE REFERENCE: 10085.500-US ; CURRENT APPLICATION NUMBER: US/09/974,300	; CURRENT FILING DATE: 2001-10-05 ; PRIOR APPLICATION NUMBER: 09/680,598	; PRIOR FILING DATE: 2000-10-06 ; PRIOR APPLICATION NUMBER: 60/279,526	; PRIOR FILING DATE: 2001-03-27 ; NUMBER OF SEQ ID NOS: 8481	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2061		; ORGANISM: Bacillus licheniformis US-09-974-300-2061	nment Scores:	3.9e-23 Length: 380.50 Matches:	nt Similarity: 52.92% Conservative: Local Similarity: 33.54% Mismatches:	22.51 % 9	.2061 (1-94		1 TTGAAAAACTATCTT	61	Db 121 AAACACAACAGGACACACAACAGATGTACCGAAAAAACCCGAAAAAAAGTCGTTGTTCAAT 180	Oy 66 TyrSerPhevalAspAlaLeuValAlaLeuAspValLysProvalGlylleAla 83	Db 181 TITGGAAIGCTIGACGCTIGAIGAGCTIGGCTIAAGCGACCGCGTIGICGCTITCCG 240	84 AspAspAsnLysLysAsnArgllelleLysProLeuArgAspLysll	Db 241 AAACAAACCTTCCGTCTTACTTGAAAAATATAAAGACAGCAAATTTGAA 291

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4 IleileAlaAspAsnAsnArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaPro 143
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9 ACGATCGACATTGAGCTTGACCAGAAGAACTACATGAACAGTTTTAAAGAAAATACCGAA 468
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AATCCTGATTACCTGTTTGTCATCGAAGGGCTGCTGGCGAAAAAGGAACAGCA 795
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F INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FERENCE: 790CTP3/US

APPLICATION NUMBER: US/10/450,763

FILING DATE: 2003-06-11

PPLICATION NUMBER: PCT/US01/08631

LILING DATE: 2001-03-30

PLICATION NUMBER: 09/540,217

HILING DATE: 2000-03-31

PELICATION NUMBER: 09/649,167

HILING DATE: 2000-08-23

ENG ID NOS: 60736

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No. US20050196754A1
ORMATION:
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                                                                                            Serlyshlaleuglylysgluglugluglylystyskrgieuglugludishsplyslys 184
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                                                                                                                                                                                                                                                                                                     IleGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLysThrIle 164
                                                                                                                                                                             85 AspasnLysLysAsnArgllelleLysProLeuArgAspLysIleGlyLysTyrThrSer 104
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    2209
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                                                                          US-10-724-972A-6352 (1-335) x US-10-450-763-7183 (1-2209)
    Length:
Matches:
Conservative:
Mismatches:
Indels:
      3.276-22
375.00
50.178
32.548
                       Percent Similarity:
Best Local Similarity:
Query Match:
D8:
Alignment Scores
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3-10-450-763-8842 Sequence 8842, Application US/10450763

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NAME/KEY: SIMILAR

LOCATION: (1)..(654)

OTHER INFORMATION: 98% homologous to Escherichia coli K12 citrate-dependent iron

OTHER INFORMATION: transport, periplasmic protein, accession number AE000499, Smith-
OTHER INFORMATION: Waterman Soore=1060.

PEATURE:
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 SerLysAlaLeuGlyLysGluGluGluGluGlyDysArgLeuGluGluHisAspLysLys 184
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Matches:
Conservative:
Mismatches:
Indels:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hyeeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLY.
FILE REFERENCE: 790CIP3/US
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: O9/540, 217
PRIOR APPLICATION NUMBER: O9/540, 217
PRIOR APPLICATION NUMBER: 09/540, 217
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE CUBEOM
SEQ ID NO 8842
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OTHER INFORMATION: n = a,t,c
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Query Match:
DB:
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205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224 ::: ::: :::	1732 G
225 GlnbeuglyPhelysGlualaLeuSerAspAspValThrLysGlyLeuSerLysTyrLeu 244	Oy 85 AspAsnLysLysAsnArgileIleLysProLeuArgAspLysIleGlyLysTyrThrSer 104
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245 LysGlyProTyrLeuGlnMetAenThrGluThrLeuSerGlnValAsnProGluArgMet 264	1852
265 PhelleMetThrAsnLysAlaSerSerAsGluProSerLeuLysGluLeuGluLysAsp 284	Qy 125 IleAlaAspAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThr 144
694 TCTATCCATGCAATTACGGTTACATCAACCACCTGTCTC735	145 IleGluLeuLysSerPheAspGlyAspTvrAsnGluAsnIleAsnaleDhefwenthrile
285 ProValTrpLysLysLeuAsnAlaValLysAsnGlnArgValAsp11eLeu 301	Db 1972 CTGCTGCTTAAGTCCCGGAAGGAAACTAGGAAATTTGCAATCTGCGGCTATCATC 2031
IGGALGECEGGGTTGCCGTTGCCGTTGGCGGTTGGCGTTCTGAAAATGACC	Oy 165 SerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184
790 GACGAAGCCGGTGAAAGTGCGAAACTGGTTCCGCAACGGCAACGCAAAGAA 849	
327	Y LEGINGANIYELYBELYBGINIE 192 Db 2092 ATGGCGCAGTGGCCCAGCTT 2115
GACGTTAAC	
SULT 29 -10-450-763-13139	US-08-781-986A-604 ; Sequence 604, Application US/08781986A
Sequence 13139, Application US/10450763 Publication No. US20050196754A1	; Publication No. US20030054436Al ; GENERAL INFORMATION: . A DETTCHARM. CLEIC
INFORMATION: ANT: Hyerg, Inc	TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SERVINGES.
OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES BFBRENCE: 790C1P3/US	
T APPLICATION NUMBER: US/10/450,763 T FILING DATE: 2003-06-11	ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
APPLICATION NUMBER: PCT/US01/08631 FILING DATE: 2001-03-30	ŏ≆
NPFLICATION NUMBER: 09/540,217 TILING DATE: 2000-03-31	ZIP: 20850
FRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage ; COMPUTER: HP Vortra 486/33
SOFTWARE: CLUE ON US: 00/36 SPQ ID NO 13139	20
LENGTH: 2799 TYPE: DNA	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/781,986A
ORGANISM: Homo sapiens FRATURE:	FILING DATE: CLASSIFICATION: 435
NAME/KEX: SIMILAR LOCATION: (181) (903) OTHER INFORMATION: 73% homologous to Mis misculing Dec. Del demons	FALOR PEPLICATION DATA: ### ### ### ### #### ###############
INFORMATION: polyprotein, accession number Y12713, Smith-Waterman Score=892.	H
	; REGISTRATION NUMBER: 30,446 ; REFERENCE/DOCKET NUMBER: PB240PP ; TELECOMMUNICATION INFORMATION:
350.00 milarity: 68.92%	; TELEPHONE: (301) 309-8504 ; TELEPAX: (301) 309-8512 ; INFORMATION FOR SEC ID NO. 601
: 46.62% Mismatches: 20.71% Indels: 24 Gaps:	0
US-10-724-972A-6352 (1-335) x US-10-450-763-13139 (1-2799)	interest acta i STRANDEDNESS: double i TOPOLOGY: linear
45 IlelysHisGluGluGlyThrThrLysValProLysHisProLysArgValValValLeu 64	5.
b// GITCAGGACGAACACGCACGTTTACACTCGAAAAAACGCCACAACGGATTGTGGTGCTG 1731	Length:
65 GluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAsp 84	SCOICE: 334.00 Matches: 67 Percent Similarity: 63.84* Conservative: 46 Best Local Similarity: 37.85\$ Mismarches: 58
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NO: 604:
                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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334.00
63.84%
37.85%
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US-08-781-986A-2556
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Best Local Similari
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470
                                                                                                                                                                                                                                                                                                                                                                                   GluThrLeuSerGlnValAsnProGluArgMetPhelleMetThrAsn---LysAlaSer 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 AAAAATAGAACGAAATTC-----ATTGATCCTGCAGTTTGGAAATCATTAAAA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 AlavaliyaAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSerArgGly 311
                                                                                                                                                                                                                                                                              234 AspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr 253
                                                                                                                                                                                                                                                                                                                                          273 SerAsnGluProSerLeuLysGluLeuGluLysAspPro---ValTrpLysLysLeuAsn 291
                                                                                                                                                                                                                   214 ProserAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSer 233
                                                                                                                                 174 GlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGluIleThr 193
                                                                                                                                                      194 MetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHis 213
                                                                      TyrasndluasnileaspalaphelysThrileSeriysalaLeuGlyLysGluGluGlu
                                                                                        GCTGTGAAAGATAACAAAGTTTATGACGTTGACCGAAATAAGTGGTTGAAATCAAGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::|||:::|||||| ||||||:::||| attatcgcaagtatatagaaaattgcagaaaaa 521
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vector 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                            (1-2115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                            US-10-724-972A-6352 (1-335) x US-08-781-986A-604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/329,624 FILING DATE: 27-Dec-2002 PRIOR APPLICATION DATA:
 Indels:
Gaps:
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FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 604, Application US/10129624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gil H. Choi
Patrick S. Dillon
19.76%
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COUNTRY: USA
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US-10-329-624-604
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    Query Match:
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254 GluThrLeuSerGlnValAsnProGluArgMetPhelleMetThrAsn---LysAlaSer 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 GCTGTGAAAGATAACAAAGTTTATGACGTTGACCGAAATAAGTGGTTGAAATCAAGGGG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2556, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 MetAspLysAsnGlnLysValLeuProAlaValAlaAlaLysSerGlyLeuLeuAlaHis 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 ProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAlaLeuSer 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 AspAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMetAsnThr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAgnGluProSerLeuLysGluLeuGluLysAgpPro---ValTrpLysLeuAsn 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlylyslyskigleuGluGluHisAspLyslleGluGluTyrLysLysGluIleThr 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY, AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMUNICATION IRFORMATION:
TELEPHONE: (240) 314-1224
TELEFRAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 604:
SEQUENCE CHARACTERISTICS:
LENGTH: 2115 base pairs
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STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329, 624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 08/781,986
FILING DATE: January 5, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
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SEQUENCE DESCRIPTION: SEQ ID
US-10-329-624-2556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                 CORRESPONDENCE ADDRESS
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Best Local Similarity:
Query Match:
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US-10-329-624-2556
; Sequence 2556, Application US/10329624
; General 2556, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 ArgileileLysProLeuArgAspLysileGlyLysTyrThrSerValGlyThrArgLys 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnProAsnLeuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 ArgHisLysGlylleTyrLysAspLeuAsnLysIleAlaProThrlleGluLeuLysSer 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
FILING DATE: APPLICATION NUMBER: US/08/781,986A

FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A

FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 30,446

REGISTRATION NUMBER: 30,446

REGISTRATION NUMBER: 30,446

RECISTRATION NUMBER: 30,446

RECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504

TELEPRAX: (301) 309-8512

INFORMATION FOR SEC 1D NO: 2556:
ENGUENCE CHARACTERISTICS:
LENGTH: 242 base pairs
TYPE: UNICIDE'S ACI'N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
               ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.86e-20
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90.00%
82.50%
19.70%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Ger
                                                                      STATE: Maryland
COUNTRY: USA
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Best Local Similarity:
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                                                                                                             20850
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90 ArgileileLysBroLeuArgAspLysileGlyLysTyrThrSerValGlyThrArgLys 109
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                                                                                                                                                                                                                                                                                                                      110 GinproAsnieuGluGluIleSerLysLeuLysProAspLeuIleIleAlaAspAsnAsn 129
                                                                                                                                                                                                                                                                                                                                           130 ArgHisLysGlyileTyrLysAspLeuAsnLysIleAlaProThrIleGluLeuLysSer 149
                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                              70 AspAlaLeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLysAsn
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                                                                                         Conservative:
Mismatches:
Indels:
                                                            Length:
Matches:
NO: 2556:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 375, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
                                                        8.86e-20
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90.00%
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290 LeuAsnAlayalLysAsnGlnArgValAspIleLeuAspArgAspLeuTrpAlaArgSer 309
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                                                                                                                                                    ------GACCTGGGGGAACGTGATTGGAATGAGTAC-----TCCATGATGGAGCTA 726
                                                                                                                                                                                                        252 AsnThrGluThrLeuSerGlnValAsnProGluArgMetPhe-----IleMetThrAsn 269
                                                                                                                                                                                                                                      270 LysalaSerSerAsnGluProSerLeuLysGluLeuGluLysAspProValTrpLysLys 289
                                                                                                                                                                                                                                                                                                                                             212 AlaHisProSerAsnSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLysGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    832 TCACCAGCAGTTCGGCAAGGTAGAACTTACGAGTTTGAAGACGAAACCTGGATGGTCGGC
                                                                                                    232 LeuSerAgpAspValThrLysGlyLeuSerLysTyrLeuLysGlyProTyrLeuGlnMet
                                634 TATGGTCCC---GAGACCTTCTGGTTCAGTTCTGGAACAAGTTGATTTT
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Matches:
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APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKINIRO
APPLICANT: OCAKI, AKI
TITLE REPRENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-16
PRIOR FILING DATE: 2000-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOROI, HANUNIKO
APPLICANT: TATELSHI, NACKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEBA, MASATO
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Matches:
Conservative:
Mismatches:
                                                                                         APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKTO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 09/377484
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SUPTWARE: PRECENTIN VEY: 3.0
SEQ ID NO 375
LENGTH: 945
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) ORGANISM: Corynebacterium glutamicum
US-09-738-626-375
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331.00
49.21%
28.57%
19.59%
                     YOKOI, HARUHIAN
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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Best Local Similarity:
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                                                                                                                                                                                                                                                            GAGGCTATTIATGATCAGCTTTCAGACATCGCACCAACCGTGATGTCCGAAGGTTCCGGC 353154
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353419 TCCTCAGAAACTTTGGGCAGATCGATGGAGACCTTATTTTCTACACCATCCCAGGATCC 353478
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                                   ThrLysyalProLysHisProLysArgvalValValLeuGluTyrSerPheValAspAla
                                                                                      LeuValAlaLeuAspValLysProValGlyIleAlaAspAspAsnLysLysAsnArgIle
                                                                                                                                                                                                                                                                                                                                                 GluGluGlyLysLysArgLeuGluGluHisAspLysLysIleGluGluTyrLysLysGlu
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1b Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
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Patent No. US20020146721A1
GENERAL INFORMATION:
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US-09-974-300-2087
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63 ValLeuGluTyrSerPheValAspAlaLeuValAlaLeuAspValLysProValGly1le 82
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147 GTACTCACGAATGAAGCGACAGAAGCGGTCGCACTTGGCGTAAAACCTGTCGGCGCC 206
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387 CCGACCGTATTTGCCGAGACATTGTCAGGGGAATGGAAAACAAC-----TTTAAG 437
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S58 GTCCGCTTTACAGATGCTGATACCCGCATCTTATCACAAAGGATCATTTGCCGGAACGATT
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                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 2087
LENGTH: 648
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 LeuSerGlnLeuGlyPhe 228
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US-10-282-122A-17083
US-10-282-122A-17083
Squence 17083, Application US/10;
Publication No. US20040029129A1;
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Best Local Similarity:
Query Match:
DB:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rompejus, Markus
APPLICANT: Rompejus, Markus
APPLICANT: Schroder, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Caelder, Oskar
APPLICANT: Geder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: UNVOINED IN HOMEOSTARIS AND ADAPTATION
TITLE OF INVENTION: LORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: LORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION NUMBER: US/10/721,922A
CURRENT APPLICATION NUMBER: US/6027177
PRIOR PILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877 TATTTAĞATTCACCAACATĞITATGTAATGATGGTĞĞTCTAACATÇTTTAAATAAAATĞ 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              598 GTAAATGAAGGTAATTTAAGTGTATTTGGTGAAGAATCAAGATTTAGTATTATACAAT 657
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                                                                                                                                                                                                                                                                                                                                                                                   185 IleGluGluTyrLysLysGluIleThrMetAspLysAsnGlnLysValLeuProAlaVal 204
                                                                                                                                                                                                                                                                                                                                                                                                                     205 AlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGlnPheLeuSer 224
313 AAAGAACCAGATTTAGAAGGTATAAAGTCGGCAAATCCAGATTTAATTATAATA---AAT 369
                                                        129 AsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAlaProThrileGluLeuLys 148
                                                                                                                                                                                                                                                                        SerlysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAspLysLys 184
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                                                                                                          370 GGAAGACAAGAAGATTTTTATGAGCAATTGTCAAAAATAGCACCAACAATAAGTACAAGT
                                                                                                                                                                   149 SerPheAspGlyAspTyrAsnGlu------AsnileAspAlaPheLysThrile
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APPLICANT: Xu, H.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

APPLICANT: Nu, HGRER: US/10/282,122A

CURRENT APPLICATION NUMBER: 00/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-09

PRIOR PILING DATE: 2000-09-06

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31 ATAGCTATTATAGGATTAGTGACAGTGTTT------GCATTAGGTGGAAGTAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 17083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-724-972A-6352 (1-335) x US-10-282-122A-17083 (1-963)
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Matches:
Conservative:
Mismatches:
Indels:
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                              Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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		7 35 7 61	1 2 1 6	1 95 1 241 115 301	135 361 155	175 472 195 532	215 589 235 634 255
Wrapper or PALM.		erSerAenSerSer 		rgilelleLyBProLeu GTTCCCCGCCTACTTG INProAsnLeuGluGlu :: :::	rgHisLysGlylleTy: ::: 	Lysgluglugluglylys 	aLysSerGlyLeuLeuAlaHisProSer
.7 .ved - See File	ive:	LeuPheValleuIleAlaThrAlaAlaCyBGlyAsnAsnSerSerSerAsnSerSer LeuPheValleuIleAlaThrAlaAlaCyBGlyAsnAsnSerSerSerAsnSerSer 	CCTGAAGTTGCCAGCACTGGATATTCAGTGGAGCACGCAATGGGCACCACCGCAAATCCT LY8HisProly8ArgValValValLeuGluTyr8erPheValAspalaLeuValAalaeu :::	ABPVALLYSPROVALGIYILEALAASPASALYSLYSASARAKGITEIJELYSPROLEU	IleSerLysLeuLysProAspLeullelleAlaAspAsnAsnArgHisLysGlyIleTyr	GluAsnileAspalaPheLysThrileSerLysAlaLeuGlyLysGluGluGluGlyLys	DYBABNGINLYBVAILGUProAlaValAlaAlaLyBSerGlyLeuLeuAlaHiBProSer GGACAAACCGCTTCAATGGTTCGATTCCGCACGACAACTTCAGGTTTATGGTCCC ABNSerTyrValGlyGlnPheLeuSerGlnLeuGlyPheLyBGluAlaLeuSerABPABP :::::
	1.8e-18 326.00 49.20% 28.30% 24.30%	lLeulleAlaThrAlaA 	::: TGCCAGCACTGGATATT TGCCAGCACTGGATATT DLY8ArgValValValL ACGCGTGTGGTCGTCACA	9ProValGlyllealaa. CCAGTCGGAGCTACGGI 111eGlyLy8TYrThrS6	IleserLysLeuLysProAspLeul ::	AspalaPheLysThrll ::: GAAATCAC GluGluHisAspLysLy TCAGACTCGGACCCC	LyBABNGINLYBVALLEUPYCALaValAlaAlaLaLyBSEr GGACAAACCGCTTCAATGGTTCGATTCCGCACGGACAC ABNSerTyrValGlyGlnPheLeuSerGlnLeuGlyPhe :::::
PRIOR APPLICATION NUMBER: DE 1993 PRIOR FILING DATE: 1999-07-09 PRIOR PLING DATE: 1999-07-09 PRIOR PLING DATE: 1999-07-09 Remaining Prior Application data NUMBER OF SEQ ID NOS: 480 SEQ ID NO 351 LENGTH: 915 TYPE: DNA PREATURE: NAME/KEY: CDS COTHER INFORMATION: RXA02052 US-10-721-922A-351	ent Scores: No.: t Similarity: ocal Similarity: Match:	17 LeuPheVa 17 LeuPheVa 1 2 CTCGGCGT	62 CCTGAAGT 56 LysHisPrc ::: 122 GAAACCCCG	76 AspvalLys ::: 182 GGAATTAC' 96 ArgAspLys 242 GCTGACGAC			196 LyBABENGIN 533 GGACAAACC 216 ABNSerTyr ::::: 590 GAGACCTTC 236 ValThrLyB 635 GGGAACGT
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730 GAAATGAATGCGGACTATATGTTCTAATTCTCAGACGATGAGAATGCCGACAATCCG 789
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                                                                                                                                                                                                                                                                                                                                                                                            202 ProAlaValAlaAlaLysSerGlyLeuLeuAlaHisProSerAsnSerTyrValGlyGln 221
                                                                                                                                                        163 ThrileSerLysAlaLeuGlyLysGluGluGluGlyLysLysArgLeuGluGluHisAsp 182
                                                                                                                                                                                                                                                 ACCGCTGTCGGCGAAAAAATGGAGCCGAACCTGGAGAAAATCCTTGAGCTGAAACCGGAT 351
                                           LeuileileAlaAspAsnAsnArgHisLysGlyIleTyrLysAspLeuAsnLysIleAla 142
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352 GTCATCCTGGCTTCAACGAAATTTCCTGATAAAGTGGTGAAAAAAACTGGGTAACATCGCG 411
                                                                                                                             143 ProThrileGluLeuLysSerPheAspGlyAspTyrAsnGluAsnIleAspAlaPheLys 162
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1 Sequence 210.7, Application US/09815242

2 Sequence 210.7, Application US/09815242

3 Sequence 210.7, Application US/09815242

4 REALICANT: Haselbeck, Robert

APPLICANT: Obleen, Kari L.

APPLICANT: Tradick, Join D.

APPLICANT: Tradick, Join D.

APPLICANT: Tradick, John D.

APPLICANT: Tradick, John D.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Dentification of Essential Genes in TITLE OF INVENTION: Light Application NUMBER: US/09/815,242

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PRIOR FILING DATE: 2000-11-27
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASLESEQ for Windows Version 4.16;
SEQ ID NO 2107
LENGTH: 321
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